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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 09:25:08 ; Search time 29.87 Seconds
(without alignments)
22.311 Million cell updates/sec

Title: BASK-853-CLAIM5

Perfect score: 24

Sequence: 1 gtxxps 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 segs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	22	91.7	10	AAG94142	Human complementar
2	22	91.7	10	AAG97971	Human complementar
3	22	91.7	10	AAG97972	Human complementar
4	22	91.7	10	AAG97973	Human complementar
5	22	91.7	10	AAG97974	Human complementar
6	22	91.7	10	AAG97975	Human complementar
7	22	91.7	38	AA58383	TSAR binding domain
8	22	91.7	50	AAU50435	Propionibacterium
9	22	91.7	52	AA53513	Human colon cancer
10	22	91.7	53	AAU47468	Propionibacterium
11	22	91.7	58	AAU48691	Propionibacterium

12	22	91.7	59	22	AAO10898	Human polypeptide
13	22	91.7	61	22	AAU62078	Propionibacterium
14	22	91.7	62	22	AAU50474	Propionibacterium
15	22	91.7	76	22	AAU61979	Propionibacterium
16	22	91.7	78	20	AAU29072	T. gondii immunoge
17	22	91.7	78	22	AAU25543	T. gondii immunoge
18	22	91.7	80	22	AAU49223	Propionibacterium
19	22	91.7	82	22	AAU49223	Propionibacterium
20	22	91.7	86	22	AAG76165	Human colon cancer
21	22	91.7	90	22	AAU90260	Human immune/haema
22	22	91.7	91	22	ABE39057	Peptide #6563 enco
23	22	91.7	91	22	AAU95131	Human reproductive
24	22	91.7	91	22	AAU59709	Human brain expres
25	22	91.7	91	22	AAU72289	Human bone marrow
26	22	91.7	91	22	AAU32548	Peptide #6585 enco
27	22	91.7	106	22	AAU90809	Human immune/haema
28	22	91.7	109	21	AAG24569	Arabidopsis thalia
29	22	91.7	110	22	AAU92684	Human digestive sy
30	22	91.7	116	20	AAU12647	Propionibacterium
31	22	91.7	118	22	AAU65364	Propionibacterium
32	22	91.7	122	22	AAU50960	Propionibacterium
33	22	91.7	157	22	AAU92476	Human protein sequ
34	22	91.7	160	21	AAU32650	Eucalyptus grandis
35	22	91.7	160	21	AAG24568	Arabidopsis thalia
36	22	91.7	166	18	AAU32476	BBC6 protein for r
37	22	91.7	168	17	AAU95975	Nucleic acid recog
38	22	91.7	173	22	AAU38749	Novel subtilisin h
39	22	91.7	173	22	AAU38776	Novel subtilisin h
40	22	91.7	173	22	AAU38780	Novel subtilisin h
41	22	91.7	173	22	AAU38787	Novel subtilisin h
42	22	91.7	173	22	AAU38804	Novel subtilisin h
43	22	91.7	173	22	AAU38810	Novel subtilisin h
44	22	91.7	173	22	AAU38835	Novel subtilisin h
45	22	91.7	173	22	AAU38843	Novel subtilisin h
46	22	91.7	173	22	AAU38869	Novel subtilisin h
47	22	91.7	175	22	ABE68003	Drosophila melanog
48	22	91.7	182	22	ABE68002	Drosophila melanog
49	22	91.7	190	22	AAU40840	Human polypeptide
50	22	91.7	194	22	AAU40065	Propionibacterium

ALIGNMENTS

RESULT 1
AAG94142
ID AAG94142 standard; Peptide; 10 AA.

AC AAG94142;

DT 18-SEP-2001 (first entry)

DE Human complementary peptide, SEQ ID NO: 336.

Human; complementary peptide; ligand; drug discovery; drug design.

Homo sapiens.

WO200142277-A2.

14-JUN-2001.

13-DEC-2000; 2000WO-GB04776.

13-DEC-1999; 99GB-0029464.

(PROT-) PROTEOM LTD.

Roberts GW, Heal JR;

WPI: 2001-408419/43.

A set of peptide ligands consisting of specific complementary peptides

PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
XX Example 4; Page 88; 646pp; English.
PS

CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;

Query Match 91.7%; Score 22; DB 22; Length 10;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 5 gtssps 10

RESULT 2
AAG97971
ID AAG97971 standard; Peptide; 10 AA.

AC AAG97971;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 4166.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04776.

XX PR 13-DEC-1999; 99GB-0029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
XX Example 6; Page 630; 646pp; English.

XX PS The invention relates to a set of complementary peptide ligands

XX CC generated from the human genome. The complementary peptides

XX CC interact with their relevant target proteins encoded in the human

XX CC genome. They can be used as reagents in drug discovery and as lead

XX CC ligands to facilitate drug design and development. The present

XX CC sequence is a complementary peptide provided in the specification.

XX SQ Sequence 10 AA;

Query Match 91.7%; Score 22; DB 22; Length 10;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 5 gtssps 10

RESULT 3
AAG97972
ID AAG97972 standard; Peptide; 10 AA.

XX AC AAG97972;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 4167.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04776.

XX PR 13-DEC-1999; 99GB-0029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
XX Example 6; Page 630; 646pp; English.

XX PS The invention relates to a set of complementary peptide ligands

XX CC generated from the human genome. The complementary peptides

XX CC interact with their relevant target proteins encoded in the human

XX CC genome. They can be used as reagents in drug discovery and as lead

XX CC ligands to facilitate drug design and development. The present

XX CC sequence is a complementary peptide provided in the specification.

XX SQ Sequence 10 AA;

Query Match 91.7%; Score 22; DB 22; Length 10;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 5 gtssps 10

RESULT 4
AAG97973
ID AAG97973 standard; Peptide; 10 AA.

XX AC AAG97973;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 4168.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

RESULT 9

AA053513
ID AAB53513 standard; Protein; 52 AA.
XX AC
XX AAB53513;
XX DT
XX 09-MAR-2001 (first entry)
XX DE Human colon cancer antigen protein sequence SEQ ID NO:1053.
XX DE Human: colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder.
XX OS
XX Homo sapiens.
XX OS
XX WO200055351-A1.
XX PN
XX 21-SEP-2000.
XX PD
XX 08-MAR-2000; 2000WO-US05883.
XX PF
XX 12-MAR-1999; 99US-0124270.
XX PR
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX Rosen CA, Ruben SM;
XX PI
XX WPI; 2000-587534/55.
XX DR
XX N-PSDB; AAC98270.
XX DR
XX Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
XX Claim 11; Page 1633; 2104pp; English.
XX PS
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 52 AA;
XX SQ

Query Match 91.7%; Score 22; DB 21; Length 52;
Best Local Similarity 66.7%; Pred. No. 2.le+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 1 gtssps 6

RESULT 10

AAU47468
ID AAU47468 standard; Protein; 53 AA.

XX

AAU47468;
XX AC
XX 27-FEB-2002 (first entry)
XX DT
XX DE
XX Propionibacterium acnes immunogenic protein #8364.
XX DE
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX OS
XX Propionibacterium acnes.
XX OS
XX WO200181581-A2.
XX PN
XX 01-NOV-2001.
XX PD
XX 20-APR-2001; 2001WO-US12865.
XX PF
XX 21-APR-2000; 2000US-199047P.
XX PR
XX 02-JUN-2000; 2000US-208841P.
XX PR
XX 07-JUL-2000; 2000US-216747P.
XX PR
XX (CORI-) CORIXA CORP.
XX PA
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX PI
XX WPI; 2001-616774/71.
XX DR
XX N-PSDB; AAS59539.
XX DR
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1; SEQ ID No 8663; 1069pp; English.
XX PS
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 53 AA;
XX SQ

Query Match 91.7%; Score 22; DB 22; Length 53;
Best Local Similarity 66.7%; Pred. No. 2.le+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 12 gtatps 17

RESULT 11
AAU48691

DE XX Propionibacterium acnes immunogenic protein #22974.
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
OS XX
XX Propionibacterium acnes.
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59623.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1; SEQ ID No 23273; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 61 AA;

Query Match 91.7%; Score 22; DB 22; Length 61;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
| | | |
Db 42 gtsps 47

RESULT 14
AAU50474
ID AAU50474 standard; Protein; 62 AA.
XX
AC AAU50474;
XX
DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #11370.
DE
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
OS
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59548.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1; SEQ ID No 11669; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 62 AA;

Query Match 91.7%; Score 22; DB 22; Length 62;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
| | | |
Db 43 gtsps 48

RESULT 15
AAU61979
ID AAU61979 standard; Protein; 76 AA.
XX
AC AAU61979;
XX

DT 27-FEB-2002 (first entry)
XX Propionibacterium acnes immunogenic protein #22875.
DE
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US12865.
XX
XX 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59621.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1; SEQ ID No 23174; 1069pp; English.
PS
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 76 AA;

Query Match 91.7%; Score 22; DB 22; Length 76;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 2 gttspss 7

RESULT 16
AAU29072
ID AAU29072 standard; Protein; 78 AA.
XX
AC AAU29072;

Query Match 91.7%; Score 22; DB 22; Length 76;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 2 gttspss 7

RESULT 16
AAU29072
ID AAU29072 standard; Protein; 78 AA.
XX
AC AAU29072;

XX 24-SEP-1999 (first entry)
DT XX
XX T. gondii immunogenic protein.
DE
XX Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
KW Toxoplasma oocyst.
XX
XX Toxoplasma gondii.
OS
XX WO9932633-A1.
PN
XX 01-JUL-1999.
PD
XX 18-DEC-1998; 98WO-US27137.
PF
XX 19-DEC-1997; 97US-0994825.
PR
XX (HESK-) HESKA CORP.
PA
XX Lutz SB, Milhausen MJ, Ng RK;
PI
XX WPI; 1999-418930/35.
DR N-PSDB; AAX91398.
DR
XX New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
PT infection caused by this microorganism
PT
XX Claim 29; Page 319-320; 381pp; English.
PS
XX The invention provides isolated Toxoplasma gondii nucleic acids that
CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,
CC immunogenic proteins and antibodies to the proteins can be used to
CC inhibit T. gondii oocyst shedding in a cat due to infection with
CC T. gondii. They can be used for preventing T. gondii infection and for
CC preventing the spread of T. gondii infection. They can also be used for
CC detecting T. gondii infection. The detection method can be used to detect
CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
CC such as Cryptosporidium oocysts and Toxoplasma oocysts.
XX
SQ Sequence 78 AA;

Query Match 91.7%; Score 22; DB 20; Length 78;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 50 gtspps 55

RESULT 17
AAU25543
ID AAU25543 standard; Protein; 78 AA.
XX
XX AAU25543;
AC
XX 17-DEC-2001 (first entry)
DT
XX T. gondii immunogenic protein PM2A18-a.
DE
XX Immunogenic protein; oocyst; faeces; enteric apicomplexa oocyst;
KW Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;
KW oocyte shedding.
XX
XX Toxoplasma gondii.
OS
XX US2001014447-A1.
PN
XX 16-AUG-2001.
PD
XX

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59545.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
PS Example 1; SEQ ID NO 10418; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 82 AA;

Query Match 91.7%; Score 22; DB 22; Length 82;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gtxxps 6
Db 33 gttaps 38
|||
|||

RESULT 20
AAG76165
ID AAG76165 standard; Protein; 86 AA.
XX
XX AAG76165;
AC
XX 03-SEP-2001 (first entry)
DT
XX Human colon cancer antigen protein SEQ ID NO:6929.
DE
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 12.
KW
XX Homo sapiens.
OS
XX WO200122920-A2.
PN
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000WO-US26524.
PF
XX 29-SEP-1999; 99US-0157137.
PR
XX 03-NOV-1999; 99US-0163280.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI WPI; 2001-235357/24.
XX
XX

DR N-PSDB; AAH35570.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 8369; 9803pp; English.
PS
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAH77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 86 AA;

Query Match 91.7%; Score 22; DB 22; Length 86;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gtxxps 6
Db 37 gttaps 42
|||
|||

RESULT 21
AAM90260
ID AAM90260 standard; Protein; 90 AA.
XX
XX AAM90260;
AC
XX 07-NOV-2001 (first entry)
DT
XX Human immune/haematopoietic antigen SEQ ID NO:17853.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
KW
XX Homo sapiens.
OS
XX WO200157182-A2.
PN
XX 09-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US01354.
PF
XX 31-JAN-2000; 2000US-0179065.
PR
XX 04-FEB-2000; 2000US-0180628.
PR
XX 24-FEB-2000; 2000US-0184664.
PR
XX 02-MAR-2000; 2000US-0186350.
PR
XX 16-MAR-2000; 2000US-0189874.
PR
XX 17-MAR-2000; 2000US-0190076.
PR
XX 18-APR-2000; 2000US-0198123.
PR
XX 19-MAY-2000; 2000US-0205515.
PR
XX 28-JUN-2000; 2000US-0209467.
PR
XX 30-JUN-2000; 2000US-0214886.
PR
XX 07-JUL-2000; 2000US-0215135.
PR
XX 07-JUL-2000; 2000US-0216647.
PR
XX 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

N-PSDB; AAK63041.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Claim 11; SEQ ID NO 17853; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (i) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 90 AA;

Query Match 91.7%; Score 22; DB 22; Length 90;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gtxxps 6
|| ||
Db 1 gtasps 6

RESULT 22

ABB39057
ID ABB39057 standard; Peptide; 91 AA.

XX
AC ABB39057;

XX
DT 04-FEB-2002 (first entry)

XX
DE Peptide #6563 encoded by human foetal liver single exon probe.

XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX
OS Homo sapiens.

XX
PN WO200157277-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US00669.

XX
PR 04-FEB-2000; 2000US-0180312.

XX
PR 26-MAY-2000; 2000US-0207456.

XX
PR 30-JUN-2000; 2000US-0608408.

XX
PR 03-AUG-2000; 2000US-0632366.

XX
PR 21-SEP-2000; 2000US-0234687.

XX
PR 27-SEP-2000; 2000US-0236359.

XX
PR 04-OCT-2000; 2000GB-0024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
XX WPT; 2001-483447/52.

XX
PT Human genome-derived single exon nucleic acid probes useful for

XX
PT analyzing gene expression in human fetal liver -

XX
PS Claim 27; SEQ ID NO 31692; 639pp + sequence listing; English.

XX
CC The invention relates to a single exon nucleic acid probe for

XX
CC measuring human gene expression in a sample derived from human foetal

XX
CC liver. The single exon nucleic acid probes may be used for predicting,

XX
CC measuring and displaying gene expression in samples derived from human

XX
CC fetal liver. The present sequence is a peptide encoded by a single exon

XX
CC nucleic acid probe of the invention.

XX
CC Note: The sequence data for this patent did not form part of the

XX
CC printed specification, but was obtained in electronic format directly

XX
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
XX Sequence 91 AA;

Query Match 91.7%; Score 22; DB 22; Length 91;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gtxxps 6
|| ||
Db 56 gtssps 61

RESULT 23

AAM95131
ID AAM95131 standard; Protein; 91 AA.

XX
AC AAM95131;

XX
DT 21-NOV-2001 (first entry)

XX
DE Human reproductive system related antigen SEQ ID NO: 3789.

XX
KW Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy.

XX
OS Homo sapiens.

XX
PN WO200155320-A2.

XX
PD 02-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US01339.

XX
PR 31-JAN-2000; 2000US-0179065.

XX
PR 04-FEB-2000; 2000US-0180628.

XX
PR 24-FEB-2000; 2000US-0184664.

XX
PR 02-MAR-2000; 2000US-0186350.

XX
PR 16-MAR-2000; 2000US-0189874.

XX
PR 17-MAR-2000; 2000US-0190076.

XX
PR 18-APR-2000; 2000US-0198123.

XX
PR 19-MAY-2000; 2000US-0205515.

XX
PR 07-JUN-2000; 2000US-0209467.

XX
PR 28-JUN-2000; 2000US-0214886.

XX
PR 30-JUN-2000; 2000US-0215135.

XX
PR 07-JUL-2000; 2000US-0216647.

XX
PR 07-JUL-2000; 2000US-0216880.

XX
PR 11-JUL-2000; 2000US-0217487.

XX
PR 11-JUL-2000; 2000US-0217496.

XX
PR 14-JUL-2000; 2000US-0218290.

XX
PR 26-JUL-2000; 2000US-0220963.

XX
PR 26-JUL-2000; 2000US-0220964.

XX
PR 14-AUG-2000; 2000US-0224518.

XX
PR 14-AUG-2000; 2000US-0224519.

XX
PR 14-AUG-2000; 2000US-0225213.

XX
PR 14-AUG-2000; 2000US-0225214.

XX
PR 14-AUG-2000; 2000US-0225266.

XX
PR 14-AUG-2000; 2000US-0225267.

XX
PR 14-AUG-2000; 2000US-0225268.

XX
PR 14-AUG-2000; 2000US-0225270.

XX
PR 14-AUG-2000; 2000US-0225447.

XX
PR 14-AUG-2000; 2000US-0225757.

XX
PR 14-AUG-2000; 2000US-0225758.

XX
PR 14-AUG-2000; 2000US-0225759.

XX
PR 18-AUG-2000; 2000US-0226279.

XX
PR 22-AUG-2000; 2000US-0226681.

XX
PR 22-AUG-2000; 2000US-0226686.

XX
PR 22-AUG-2000; 2000US-0227182.

XX
PR 23-AUG-2000; 2000US-0227009.

XX
PR 30-AUG-2000; 2000US-0228924.

XX
PR 01-SEP-2000; 2000US-0229287.

XX
PR 01-SEP-2000; 2000US-0229343.

XX
PR 01-SEP-2000; 2000US-0229345.

XX
PR 05-SEP-2000; 2000US-0229509.

XX
PR 06-SEP-2000; 2000US-0229513.

XX
PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 12-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0233423.
PR 21-SEP-2000; 2000US-0233474.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.

PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
DR N-PSDB; AAL01101.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen -
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 11; SEQ ID NO 3789; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
XX Sequence 91 AA;
XX
Query Match 91.7%; Score 22; DB 22; Length 91;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 gtxxps 6
Db 16 gtxtps 21
RESULT 24
ARM59709 standard; Protein; 91 AA.
ID AAM59709;
XX
AC AAM59709;
XX
DT 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 31814.
DE Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00667.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR

PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
DR Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX Example 4; SEQ ID NO: 31814; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX Sequence 91 AA;
SQ

Query Match 91.7%; Score 22; DB 22; Length 91;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
||| ||
Db 56 gtsps 61

RESULT 25
AAM72289
ID AAM72289 standard; Protein; 91 AA.
XX AC AAM72289;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32595.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00668.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX Example 4; SEQ ID NO: 32595; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX Sequence 91 AA;
SQ

Query Match 91.7%; Score 22; DB 22; Length 91;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
||| ||
Db 56 gtsps 61

RESULT 26
AAM32548
ID AAM32548 standard; Protein; 91 AA.
XX AC AAM32548;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #6585 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Claim 27; SEQ ID NO 32817; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP;
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX Sequence 91 AA;
SQ

Query Match 91.7%; Score 22; DB 22; Length 91;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 56 gtsps 61

RESULT 27
AAM90809
ID AAM90809 standard; Protein; 106 AA.
AC AAM90809;
XX
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen SEQ ID NO:18402.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190976.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.

06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
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PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX N-PSDB; AAK63590.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Claim 11; SEQ ID NO 18402; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 106 AA;

Query Match 91.7%; Score 22; DB 22; Length 106;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 gtxxps 6
Db 37 gtsaps 42
|| ||
|| ||
RESULT 28
AAG24569
ID AAG24569 standard; Protein; 109 AA.
XX
AC AAG24569;
XX
XX 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28293.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
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XX 21-APR-1999; 99US-0130449.
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XX 28-APR-1999; 99US-0131449.
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XX 04-MAY-1999; 99US-0132484.
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XX 04-JUN-1999; 99US-0137502.
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XX 21-JUN-1999; 99US-0139817.

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PR 02-AUG-1999; 99US-0146386.
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PR 05-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
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PR 30-AUG-1999; 99US-01511303.
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PR 01-SEP-1999; 99US-0151930.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
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PR 14-OCT-1999; 99US-0159331.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 91.7%; Score 22; DB 21; Length 109;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gtxxps 6
|||
Db 71 gtttpps 76

RESULT 29
AAM92684
ID AAM92684 standard; Protein; 110 AA.

XX AC AAM92684;

XX DT 06-NOV-2001 (first entry)

XX DE Human digestive system antigen SEQ ID NO: 2033.

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX digestive system disorder; Meckel's diverticulum.
OS Homo sapiens.

XX WO200155314-A2.
PN 02-AUG-2001.
PD
XX
PF 17-JAN-2001; 2001WO-US01324.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-502630/55.
 DR N-PSDB; AAK88457.
 XX
 PT Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases -
 XX
 PS Claim 11; SEQ ID NO 2033; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a digestive system antigen of
 CC the invention.
 XX
 SQ Sequence 110 AA;
 Query Match 91.7%; Score 22; DB 22; Length 110;
 Best Local Similarity 66.7%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gtxxps 6
 || ||
 Db 13 gtsaps 18
 RESULT 30
 AAY12647
 ID AAY12647 standard; Protein; 116 AA.
 XX
 AC AAY12647;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE Human 5' EST secreted protein SEQ ID NO: 312 from WO 9906553.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; antiinflammatory; tumour inhibition; antitumour.
 XX
 OS Homo sapiens.
 XX
 PN WO9906553-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB01237.
 XX
 PR 01-AUG-1997; 97US-0905051.
 XX
 PA (GEST) GENSET.
 XX
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;
 XX
 DR WPI; 1999-153783/13.
 DR N-PSDB; AAX41505.
 XX
 PT New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries derived from umbilical cord, lymph ganglia,
 PT lymphocytes and placental tissue
 XX
 PS Claim 34; Page 397-398; 411pp; English.
 XX
 CC AAX41379 to AAX41526 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12521 to

CC AAY12668, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, antiinflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.
 XX
 SQ Sequence 116 AA;
 Query Match 91.7%; Score 22; DB 20; Length 116;
 Best Local Similarity 66.7%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 gtxxps 6
 || ||
 Db 53 gtsaps 58
 RESULT 31
 AAU65364
 ID AAU65364 standard; Protein; 118 AA.
 XX
 AC AAU65364;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #26260.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59666.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 26559; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 118 AA;

Query Match 91.7%; Score 22; DB 22; Length 118;
 Best Local Similarity 66.7%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 111 gtatps 116

RESULT 32

AAU50960
 ID AAU50960 standard; Protein; 122 AA.

XX AAU50960;

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #11856.

DE SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-195047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX N-PSDB; AAS59549.

XX WPI; 2001-616774/71.

XX Example 1; SEQ ID No 12155; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 122 AA;

Query Match 91.7%; Score 22; DB 22; Length 122;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 18 gtttps 23

RESULT 33

AAB92476

ID AAB92476 standard; Protein; 157 AA.

XX AAB92476;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:10552.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

XX full-length cDNAs defined in the specification, and for the detection
 CC and/or diagnosis of the abnormality of the proteins encoded by the
 CC full-length cDNAs -
 CC Claim 8; SEQ ID 10552; 2537pp + CD ROM; English.
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX SQ Sequence 157 AA;

Query Match 91.7%; Score 22; DB 22; Length 157;

Best Local Similarity 66.7%; Pred. No. 5.7e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

Db 76 gtaaps 81

RESULT 34

AAB32650

ID AAB32650 standard; Protein; 160 AA.

XX AC AAB32650;

XX DT 25-JAN-2001 (first entry)

XX DE Eucalyptus grandis transcription factor protein sequence #108.

XX KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

XX KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;

XX KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;

XX KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;

XX KW type 2 Cys2His2; CCAAT box element; MYB.

XX OS Eucalyptus grandis.

XX PN WO200053724-A2.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-US06112.

XX PR 11-MAR-1999; 99US-0266513.

XX PR 18-AUG-1999; 99US-0149485.

XX XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX PI Wood M, McGrath A, Shenk MA, Glenn M;

XX WPI; 2000-579369/54.

XX

PT New isolated polynucleotide encoding a plant transcription factor for

PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,

PT having modified gene expression or modified activity of a polypeptide

PT

XX

PS Claim 8; Page 243; 747pp; English.

XX

CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
 CC Cys2His2, CCAAT box elements and MYB.

XX SQ Sequence 160 AA;

Query Match 91.7%; Score 22; DB 21; Length 160;

Best Local Similarity 66.7%; Pred. No. 5.8e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

Db 112 gtaaps 117

RESULT 35

AAG24568

ID AAG24568 standard; Protein; 160 AA.

XX AC AAG24568;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 28292.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151086.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 91.7%; Score 22; DB 21; Length 160;
 Best Local Similarity 66.7%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 122 gttgts 127

RESULT 36
 AAW32476
 ID AAW32476 standard; Protein; 166 AA.

XX AC AAW32476;
 XX DT 15-JAN-1998 (first entry)
 XX DE BBC6 protein for regulating cell death.

XX KW BBC6 gene; cell death; cell cycle; Bcl2; human.
 XX OS Homo sapiens.

XX PN US5663316-A.
 XX PD 02-SEP-1997.
 XX PF 18-JUN-1996; 96US-0665617.
 XX PR 18-JUN-1996; 96US-0665617.
 XX PA (CLON-) CLONTECH LAB INC.
 XX PI Xu Dong Y;
 XX DR WPI; 1997-447980/41.
 XX DR N-PSDB; AAT91561.

XX PT Isolated BBC6 gene - encodes a protein that regulates cell death
 through interaction with Bcl-2
 XX PS Claim 1; Column 11-12; 7pp; English.

XX CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BBC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BBC6 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 91.7%; Score 22; DB 18; Length 166;
 Best Local Similarity 66.7%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 160 gtaaps 165

RESULT 37

AAR95975
 ID AAR95975 standard; peptide; 168 AA.

XX AC AAR95975;
 XX DT 19-FEB-1997 (first entry)
 XX DE Nucleic acid recognition unit #11.

XX KW Target binding assembly; nucleic acid recognition unit: NF-kappa-B; SPI;
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
 KW virus.

XX OS Synthetic.

XX PN WO9617956-A2.

XX PD 13-JUN-1996.

XX PF 07-DEC-1995; 95WO-US15944.

XX PR 09-DEC-1994; 94US-0353476.

XX PA (GENE-) GENE POOL INC.

XX PI Weininger AM, Weininger S;

XX DR WPI; 1996-287199/29.

XX PT Probe nucleic acids, target binding assemblies, etc - for detection
 PT and localisation of specific nucleic acid sequences, esp. HIV and
 PT HPV

XX PS Claim 14; Page 97-98; 172pp; English.

XX CC AAR95965-R95993 represent the nucleic acid recognition units (NAR) of
 CC target binding assemblies (TBA) of the invention. These NARs are
 CC selected from NF-kappa-B, SPI, TATA, human papillomavirus (HPV) E2, HPV
 CC LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. This
 CC sequence represents a SPI sequence NAR. The TBA is recognised by the
 CC target binding region (TBR) of a probe of the invention. The probe of
 CC the invention contains a TBR, a booster binding region (BBR), and an
 CC optional support or attachment (OSA). The TBA contains at least one
 CC NAR, and optionally a linker sequence, an assembly sequence, an
 CC asymmetry sequence, a nuclear localisation signal sequence, and an OSA.
 CC The assembly sequence and asymmetry sequences are responsible for the
 CC folding and association of the NARs. The linker sequence is an
 CC oligopeptide, which does not interfere with NAR function, but provides
 CC stability and control over the spacing of the NAR from the rest of the
 CC TBA. The OSA is an attached support or indicator, or other means of
 CC localisation of the probe. The probe can be used in a method for
 CC detecting or localising a specific target nucleic acid sequence (TNA).
 CC The method is highly sensitive, and has a high degree of specificity.
 CC The method can be used for detecting specific nucleic acid sequences,
 CC including those found in human cells, in HIV, HPV, and other nucleic acid
 CC containing systems, including bacteria and viruses.

XX SQ Sequence 168 AA;

Query Match 91.7%; Score 22; DB 17; Length 168;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 119 gtaaps 124

RESULT 38
 AAU38749

ID AAU38749 standard; Protein; 173 AA.
XX AC AAU38749;
XX DT 19-DEC-2001 (first entry)
XX DE Novel subtilisin homologue #6.
XX KW Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
XX KW contact lens cleansing solution; dry cleaning.
XX OS Bacillus sp.
XX PN WO200175087-A2.
XX PD 11-OCT-2001.
XX PF 02-APR-2001; 2001WO-US10781.
XX PR 03-APR-2000; 2000US-194143P.
XX PA (MAXY-) MAXYGEN INC.
XX PI Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
XX PI Minshull J;
XX DR WPI; 2001-616689/71.
XX DR N-PSDB; AAS56604.
XX PT Novel subtilisin homologue polypeptides having improved endo-protease
XX PT activity relative to mature Savinase subtilisin polypeptide, useful as
XX PT component of cleaning solutions e.g. laundry detergents, dry cleaning
XX PS Claim 1; Page 103; 138pp; English.
XX CC The invention relates to an isolated polypeptide with improved endo-
XX CC protease activity relative to subtilisin homologue polypeptide, Savinase
XX CC (RTM). The invention also relates to an integrated system comprising a
XX CC computer or computer readable medium comprising a database comprising one
XX CC or more sequence records. Each record comprises one or more character
XX CC string corresponding to a nucleic acid or protein sequence of AAS56599-
XX CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
XX CC comprises a user input interface allowing a user to selectively
XX CC one or more sequence record. The integrated system is useful for
XX CC presenting information pertaining to one of several sequence records
XX CC stored in a database. The method involves determining a list of one or
XX CC more character strings corresponding to the sequence or its subsequence,
XX CC and displaying the selected character strings or aligning the selected
XX CC character string with an additional character string. The method
XX CC further involves displaying an alignment of the selected character
XX CC string with the additional character string, and displaying the list.
XX CC The polynucleotides are useful as probes, primers, sense and antisense
XX CC nucleotides. The subtilisin homologue polypeptides are useful for
XX CC producing antibodies which have diagnostic uses related to the activity,
XX CC distribution and expression of subtilisin homologues. The subtilisin
XX CC homologue polypeptides are used in compositions that serve as cleaning
XX CC solutions in a wide variety of applications including laundry detergents,
XX CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
XX CC represent the amino acid sequences of novel subtilisin homologues of the
XX CC invention.

Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 71 gtsaps 76

RESULT 39
AAU38776
ID AAU38776 standard; Protein; 173 AA.
XX AC AAU38776;
XX DT 19-DEC-2001 (first entry)
XX DE Novel subtilisin homologue #33.
XX KW Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
XX KW contact lens cleansing solution; dry cleaning.
XX OS Bacillus sp.
XX PN WO200175087-A2.
XX PD 11-OCT-2001.
XX PF 02-APR-2001; 2001WO-US10781.
XX PR 03-APR-2000; 2000US-194143P.
XX PA (MAXY-) MAXYGEN INC.
XX PI Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
XX PI Minshull J;
XX DR WPI; 2001-616689/71.
XX DR N-PSDB; AAS56631.
XX PT Novel subtilisin homologue polypeptides having improved endo-protease
XX PT activity relative to mature Savinase subtilisin polypeptide, useful as
XX PT component of cleaning solutions e.g. laundry detergents, dry cleaning
XX PS Claim 1; Page 106; 138pp; English.
XX CC The invention relates to an isolated polypeptide with improved endo-
XX CC protease activity relative to subtilisin homologue polypeptide, Savinase
XX CC (RTM). The invention also relates to an integrated system comprising a
XX CC computer or computer readable medium comprising a database comprising one
XX CC or more sequence records. Each record comprises one or more character
XX CC string corresponding to a nucleic acid or protein sequence of AAS56599-
XX CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
XX CC comprises a user input interface allowing a user to selectively
XX CC one or more sequence record. The integrated system is useful for
XX CC presenting information pertaining to one of several sequence records
XX CC stored in a database. The method involves determining a list of one or
XX CC more character strings corresponding to the sequence or its subsequence,
XX CC and displaying the selected character strings or aligning the selected
XX CC character string with an additional character string. The method
XX CC further involves displaying an alignment of the selected character
XX CC string with the additional character string, and displaying the list.
XX CC The polynucleotides are useful as probes, primers, sense and antisense
XX CC nucleotides. The subtilisin homologue polypeptides are useful for
XX CC producing antibodies which have diagnostic uses related to the activity,
XX CC distribution and expression of subtilisin homologues. The subtilisin
XX CC homologue polypeptides are used in compositions that serve as cleaning
XX CC solutions in a wide variety of applications including laundry detergents,
XX CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
XX CC represent the amino acid sequences of novel subtilisin homologues of the
XX CC invention.

Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 71 gtsaps 76

RESULT 40
AAU38780
ID AAU38780 standard; Protein; 173 AA.

AC AAU38780;

XX 19-DEC-2001 (first entry)

XX Novel subtilisin homologue #37.

XX Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
KW contact lens cleansing solution; dry cleaning.

XX Bacillus sp.

XX WO200175087-A2.

XX 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10781.

XX 03-APR-2000; 2000US-194143P.

XX (MAXY-) MAXYGEN INC.

XX Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
PI Minshull J;

XX WPI: 2001-616689/71.

XX N-PSDB; AAS56635.

XX Novel subtilisin homologue polypeptides having improved endo-protease
PT activity relative to mature Savinase subtilisin polypeptide, useful as
PT component of cleaning solutions e.g. laundry detergents, dry cleaning
PT .

PS Claim 1; Page 106; 138pp; English.

XX The invention relates to an isolated polypeptide with improved endo-
CC protease activity relative to subtilisin homologue polypeptide, Savinase
CC (RTM). The invention also relates to an integrated system comprising a
CC computer or computer readable medium comprising a database comprising one
CC or more sequence records. Each record comprises one or more character
CC string corresponding to a nucleic acid or protein sequence of AAS56599-
CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
CC comprises a user input interface allowing a user to selectively
CC one or more sequence record. The integrated system is useful for
CC presenting information pertaining to one of several sequence records
CC stored in a database. The method involves determining a list of one or
CC more character strings corresponding to the sequence or its subsequence,
CC determining which character strings of the list are selected by a user,
CC and displaying the selected character strings or aligning the selected
CC character string with an additional character string. The method
CC further involves displaying an alignment of the selected character
CC string with the additional character string, and displaying the list.
CC The polynucleotides are useful as probes, primers, sense and antisense
CC nucleotides. The subtilisin homologue polypeptides are useful for
CC producing antibodies which have diagnostic uses related to the activity,
CC distribution and expression of subtilisin homologues. The subtilisin
CC homologue polypeptides are used in compositions that serve as cleaning
CC solutions in a wide variety of applications including laundry detergents,
CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
CC represent the amino acid sequences of novel subtilisin homologues of the
CC invention.

XX Sequence 173 AA;

SQ

Query Match 91.7%; Score 22; DB 22; Length 173;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 71 gtsaps 76

RESULT 41

AAU38787
ID AAU38787 standard; Protein; 173 AA.

XX AC AAU38787;

XX 19-DEC-2001 (first entry)

XX Novel subtilisin homologue #44.

XX Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
KW contact lens cleansing solution; dry cleaning.

XX Bacillus sp.

XX WO200175087-A2.

XX 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10781.

XX 03-APR-2000; 2000US-194143P.

XX (MAXY-) MAXYGEN INC.

XX Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
PI Minshull J;

XX WPI: 2001-616689/71.

XX N-PSDB; AAS56642.

XX Novel subtilisin homologue polypeptides having improved endo-protease
PT activity relative to mature Savinase subtilisin polypeptide, useful as
PT component of cleaning solutions e.g. laundry detergents, dry cleaning
PT .

PS Claim 1; Page 107; 138pp; English.

XX The invention relates to an isolated polypeptide with improved endo-
CC protease activity relative to subtilisin homologue polypeptide, Savinase
CC (RTM). The invention also relates to an integrated system comprising a
CC computer or computer readable medium comprising a database comprising one
CC or more sequence records. Each record comprises one or more character
CC string corresponding to a nucleic acid or protein sequence of AAS56599-
CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
CC comprises a user input interface allowing a user to selectively
CC one or more sequence record. The integrated system is useful for
CC presenting information pertaining to one of several sequence records
CC stored in a database. The method involves determining a list of one or
CC more character strings corresponding to the sequence or its subsequence,
CC determining which character strings of the list are selected by a user,
CC and displaying the selected character strings or aligning the selected
CC character string with an additional character string. The method
CC further involves displaying an alignment of the selected character
CC string with the additional character string, and displaying the list.
CC The polynucleotides are useful as probes, primers, sense and antisense
CC nucleotides. The subtilisin homologue polypeptides are useful for
CC producing antibodies which have diagnostic uses related to the activity,
CC distribution and expression of subtilisin homologues. The subtilisin
CC homologue polypeptides are used in compositions that serve as cleaning
CC solutions in a wide variety of applications including laundry detergents,
CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
CC represent the amino acid sequences of novel subtilisin homologues of the

CC invention.
XX Sequence 173 AA;
SQ

Query Match 91.7%; Score 22; DB 22; Length 173;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 71 gtsps 76

RESULT 42
AAU38804
ID AAU38804 standard; Protein; 173 AA.
XX
AC AAU38804;
XX
DT 19-DEC-2001 (first entry)
XX
DE Novel subtilisin homologue #61.
XX
KW Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
KW contact lens cleansing solution; dry cleaning.
XX
OS Bacillus sp.
XX
PN WO200175087-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US10781.
XX
PR 03-APR-2000; 2000US-194143P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
PI Minshull J;
XX
XX WPI; 2001-616689/71.
DR N-PSDB; AAS56659.
XX
Novel subtilisin homologue polypeptides having improved endo-protease
PT activity relative to mature Savinase subtilisin polypeptide, useful as
PT component of cleaning solutions e.g. laundry detergents, dry cleaning
PT

Claim 1; Page 109; 138pp; English.
XX
XX The invention relates to an isolated polypeptide with improved endo-
XX protease activity relative to subtilisin homologue polypeptide, Savinase
XX (RTM). The invention also relates to an integrated system comprising a
XX computer or computer readable medium comprising a database comprising one
XX or more sequence records. Each record comprises one or more character
XX string corresponding to a nucleic acid or protein sequence of AAS56599-
XX AAS56728 or AAU38744-AAU38873 respectively. The integrated system
XX comprises a user input interface allowing a user to selectively
XX one or more sequence record. The integrated system is useful for
XX presenting information pertaining to one of several sequence records
XX stored in a database. The method involves determining a list of one or
XX more character strings corresponding to the sequence or its subsequence,
XX determining which character strings of the list are selected by a user,
XX and displaying the selected character strings or aligning the selected
XX character string with an additional character string. The method
XX further involves displaying an alignment of the selected character
XX string with the additional character string, and displaying the list.
XX The polynucleotides are useful as probes, primers, sense and antisense
XX nucleotides. The subtilisin homologue polypeptides are useful for
XX producing antibodies which have diagnostic uses related to the activity,
XX distribution and expression of subtilisin homologues. The subtilisin

CC homologue polypeptides are used in compositions that serve as cleaning
CC solutions in a wide variety of applications including laundry detergents,
CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
CC represent the amino acid sequences of novel subtilisin homologues of the
CC invention.
XX
SQ Sequence 173 AA;
XX

Query Match 91.7%; Score 22; DB 22; Length 173;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 71 gtsaps 76

RESULT 43
AAU38810
ID AAU38810 standard; Protein; 173 AA.
XX
AC AAU38810;
XX
DT 19-DEC-2001 (first entry)
XX
DE Novel subtilisin homologue #67.
XX
KW Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
KW contact lens cleansing solution; dry cleaning.
XX
OS Bacillus sp.
XX
PN WO200175087-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US10781.
XX
PR 03-APR-2000; 2000US-194143P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
PI Minshull J;
XX
XX WPI; 2001-616689/71.
DR N-PSDB; AAS56665.
XX
Novel subtilisin homologue polypeptides having improved endo-protease
PT activity relative to mature Savinase subtilisin polypeptide, useful as
PT component of cleaning solutions e.g. laundry detergents, dry cleaning
PT

Claim 1; Page 110; 138pp; English.
XX
XX The invention relates to an isolated polypeptide with improved endo-
XX protease activity relative to subtilisin homologue polypeptide, Savinase
XX (RTM). The invention also relates to an integrated system comprising one
XX computer or computer readable medium comprising a database comprising one
XX or more sequence records. Each record comprises one or more character
XX string corresponding to a nucleic acid or protein sequence of AAS56599-
XX AAS56728 or AAU38744-AAU38873 respectively. The integrated system
XX comprises a user input interface allowing a user to selectively
XX one or more sequence record. The integrated system is useful for
XX presenting information pertaining to one of several sequence records
XX stored in a database. The method involves determining a list of one or
XX more character strings corresponding to the sequence or its subsequence,
XX determining which character strings of the list are selected by a user,
XX and displaying the selected character strings or aligning the selected
XX character string with an additional character string. The method
XX further involves displaying an alignment of the selected character
XX string with the additional character string, and displaying the list.

CC The polynucleotides are useful as probes, primers, sense and antisense
 CC nucleotides. The subtilisin homologue polypeptides are useful for
 CC producing antibodies which have diagnostic uses related to the activity,
 CC distribution and expression of subtilisin homologues. The subtilisin
 CC homologue polypeptides are used in compositions that serve as cleaning
 CC solutions in a wide variety of applications including laundry detergents,
 CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
 CC represent the amino acid sequences of novel subtilisin homologues of the
 CC invention.

XX Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;

Best Local Similarity 66.7%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

DB 71 gtsaps 76

RESULT 44

AAU38835
 ID AAU38835 standard; Protein; 173 AA.

XX AAU38835;

DT 19-DEC-2001 (first entry)

XX Novel subtilisin homologue #92.

Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
 contact lens cleansing solution; dry cleaning.

OS Bacillus sp.

XX WO200175087-A2.

PN 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10781.

PR 03-APR-2000; 2000US-194143P.

XX (MAXY-) MAXYGEN INC.

XX Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
 PI Minshull J;

XX WPI; 2001-616689/71.

DR N-PSDB; AAS56690.

XX Novel subtilisin homologue polypeptides having improved endo-protease
 PT activity relative to mature Savinase subtilisin polypeptide, useful as
 PT component of cleaning solutions e.g. laundry detergents, dry cleaning

PS Claim 1; Page 113; 138pp; English.

XX The invention relates to an isolated polypeptide with improved endo-
 CC protease activity relative to subtilisin homologue polypeptide, Savinase
 CC (RTM). The invention also relates to an integrated system comprising a
 CC computer or computer readable medium comprising a database comprising one
 CC or more sequence records. Each record comprises one or more character
 CC string corresponding to a nucleic acid or protein sequence of AAS56599-
 CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
 CC comprises a user input interface allowing a user to selectively
 CC one or more sequence record. The integrated system is useful for
 CC presenting information pertaining to one of several sequence records
 CC stored in a database. The method involves determining a list of one or
 CC more character strings corresponding to the sequence or its subsequence,
 CC determining which character strings of the list are selected by a user,

CC and displaying the selected character strings or aligning the selected
 CC character string with an additional character string. The method
 CC further involves displaying an alignment of the selected character
 CC string with the additional character string, and displaying the list.
 CC The polynucleotides are useful as probes, primers, sense and antisense
 CC nucleotides. The subtilisin homologue polypeptides are useful for
 CC producing antibodies which have diagnostic uses related to the activity,
 CC distribution and expression of subtilisin homologues. The subtilisin
 CC homologue polypeptides are used in compositions that serve as cleaning
 CC solutions in a wide variety of applications including laundry detergents,
 CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
 CC represent the amino acid sequences of novel subtilisin homologues of the
 CC invention.

XX Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;

Best Local Similarity 66.7%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

DB 71 gtsaps 76

RESULT 45

AAU38843
 ID AAU38843 standard; Protein; 173 AA.

XX AAU38843;

DT 19-DEC-2001 (first entry)

XX Novel subtilisin homologue #100.

Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;
 contact lens cleansing solution; dry cleaning.

OS Bacillus sp.

XX WO200175087-A2.

PN 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10781.

PR 03-APR-2000; 2000US-194143P.

XX (MAXY-) MAXYGEN INC.

XX Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;
 PI Minshull J;

XX WPI; 2001-616689/71.

DR N-PSDB; AAS56698.

XX Novel subtilisin homologue polypeptides having improved endo-protease
 PT activity relative to mature Savinase subtilisin polypeptide, useful as
 PT component of cleaning solutions e.g. laundry detergents, dry cleaning

PS Claim 1; Page 114; 138pp; English.

XX The invention relates to an isolated polypeptide with improved endo-
 CC protease activity relative to subtilisin homologue polypeptide, Savinase
 CC (RTM). The invention also relates to an integrated system comprising a
 CC computer or computer readable medium comprising a database comprising one
 CC or more sequence records. Each record comprises one or more character
 CC string corresponding to a nucleic acid or protein sequence of AAS56599-
 CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
 CC comprises a user input interface allowing a user to selectively
 CC one or more sequence record. The integrated system is useful for

CC presenting information pertaining to one of several sequence records
 CC stored in a database. The method involves determining a list of one or
 CC more character strings corresponding to the sequence or its subsequence,
 CC determining which character strings of the list are selected by a user,
 CC and displaying the selected character strings or aligning the selected
 CC character string with an additional character string. The method
 CC further involves displaying an alignment of the selected character
 CC string with the additional character string, and displaying the list.
 CC The polynucleotides are useful as probes, primers, sense and antisense
 CC nucleotides. The subtilisin homologue polypeptides are useful for
 CC producing antibodies which have diagnostic uses related to the activity,
 CC distribution and expression of subtilisin homologues. The subtilisin
 CC homologue polypeptides are used in compositions that serve as cleaning
 CC solutions in a wide variety of applications including laundry detergents,
 CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
 CC represent the amino acid sequences of novel subtilisin homologues of the
 CC invention.

XX Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;

Best Local Similarity 66.7%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 71 gtspps 76

RESULT 46

AAU38869

ID AAU38869 standard; Protein; 173 AA.

AC AAU38869;

DT 19-DEC-2001 (first entry)

XX Novel subtilisin homologue #126.

DE Subtilisin; Savinase; diagnostic; cleaning solution; laundry detergent;

KW contact lens cleansing solution; dry cleaning.

KW Bacillus sp.

OS WO200175087-A2.

XX 11-OCT-2001.

XX 02-APR-2001; 2001WO-US10781.

XX 03-APR-2000; 2000US-194143P.

XX (MAXY-) MAXYGEN INC.

XX Ness JE, Welch M, Giver LJ, Cherry JR, Borchert TV, Stemmer WPC;

PI Minshull J;

XX WPI: 2001-616689/71.

DR N-PSDB; AAS56724.

XX Novel subtilisin homologue polypeptides having improved endo-protease

PT activity relative to mature Savinase subtilisin polypeptide, useful as

PT component of cleaning solutions e.g. laundry detergents, dry cleaning

PT .

XX Claim 1; Page 117; 138pp; English.

XX The invention relates to an isolated polypeptide with improved endo-

CC protease activity relative to subtilisin homologue polypeptide, Savinase

CC (RPM). The invention also relates to an integrated system comprising a

CC computer or computer readable medium comprising a database comprising one

CC or more sequence records. Each record comprises one or more character

CC string corresponding to a nucleic acid or protein sequence of AAS56599-
 CC AAS56728 or AAU38744-AAU38873 respectively. The integrated system
 CC comprises a user input interface allowing a user to selectively
 CC one or more sequence record. The integrated system is useful for
 CC presenting information pertaining to one of several sequence records
 CC stored in a database. The method involves determining a list of one or
 CC more character strings corresponding to the sequence or its subsequence,
 CC determining which character strings of the list are selected by a user,
 CC and displaying the selected character strings or aligning the selected
 CC character string with an additional character string. The method
 CC further involves displaying an alignment of the selected character
 CC string with the additional character string, and displaying the list.
 CC The polynucleotides are useful as probes, primers, sense and antisense
 CC nucleotides. The subtilisin homologue polypeptides are useful for
 CC producing antibodies which have diagnostic uses related to the activity,
 CC distribution and expression of subtilisin homologues. The subtilisin
 CC homologue polypeptides are used in compositions that serve as cleaning
 CC solutions in a wide variety of applications including laundry detergents,
 CC contact lens cleansing solutions, and dry cleaning. AAU38744-AAU38874
 CC represent the amino acid sequences of novel subtilisin homologues of the
 CC invention.

SQ Sequence 173 AA;

Query Match 91.7%; Score 22; DB 22; Length 173;

Best Local Similarity 66.7%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 71 gtspps 76

RESULT 47

ABB68003

ID ABB68003 standard; Protein; 175 AA.

XX ABB68003;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 30801.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI: 2001-656860/75.

DR N-PSDB; ABL12106.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions .

XX Disclosure; SEQ ID NO 30801; 21pp + Sequence Listing; English.

PS The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC specification.
 XX Sequence 190 AA;
 SQ Sequence 194 AA;

Query Match 91.7%; Score 22; DB 22; Length 190;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 39 gtstps 44

RESULT 50
 AAU40065
 ID AAU40065 standard; Protein; 194 AA.
 XX
 AC AAU40065;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #961.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 XX 20-APR-2001; 2001WO-US12865.
 PF
 XX 21-APR-2000; 2000US-199047P.
 PR
 PR 02-JUN-2000; 2000US-208841P.
 PR
 XX 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 PI
 XX WPI; 2001-616774/71.
 DR
 DR N-PSDB; AAS59510.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 XX Example 1; SEQ ID No 1260; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 194 AA;

Query Match 91.7%; Score 22; DB 22; Length 194;
 Best Local Similarity 66.7%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 48 gtssps 53

Search completed: September 3, 2002, 09:26:28
 Job time: 80 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2002, 09:25:08 ; Search time 12.98 seconds
(without alignments)
11.291 Million cell updates/sec

Title: BASK-853-CLAIM5
Perfect score: 24
Sequence: 1 gtxxps 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCUUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	91.7	38	1 US-08-176-500-41	Sequence 41, Appl
2	22	91.7	38	1 US-08-471-052A-41	Sequence 41, Appl
3	22	91.7	38	1 US-08-189-331-41	Sequence 41, Appl
4	22	91.7	38	2 US-08-471-939-41	Sequence 41, Appl
5	22	91.7	38	2 US-08-471-800-41	Sequence 41, Appl
6	22	91.7	38	2 US-08-471-068-41	Sequence 41, Appl
7	22	91.7	166	1 US-08-665-617-2	Sequence 2, Appl
8	22	91.7	168	2 US-08-353-476-73	Sequence 73, Appl
9	22	91.7	241	2 US-08-353-476-116	Sequence 116, App
10	22	91.7	273	2 US-08-353-476-112	Sequence 112, App
11	22	91.7	294	4 US-09-372-422A-40	Sequence 40, Appl
12	22	91.7	1050	4 US-09-428-711A-16	Sequence 16, Appl
13	21	87.5	40	5 PCN-US96-08730-14	Sequence 14, Appl
14	21	87.5	56	2 US-08-537-400-32	Sequence 32, Appl
15	21	87.5	153	4 US-09-228-986-83	Sequence 83, Appl
16	21	87.5	170	2 US-08-483-101-3	Sequence 3, Appl
17	21	87.5	170	3 US-09-081-180-5	Sequence 5, Appl
18	21	87.5	170	3 US-09-040-786-5	Sequence 5, Appl
19	21	87.5	225	1 US-08-290-979A-8	Sequence 8, Appl
20	21	87.5	295	2 US-08-481-956A-9	Sequence 9, Appl
21	21	87.5	295	2 US-08-629-291A-9	Sequence 9, Appl
22	21	87.5	295	2 US-08-658-335B-9	Sequence 9, Appl
23	21	87.5	334	2 US-08-997-080-45	Sequence 45, Appl
24	21	87.5	334	2 US-08-997-362-45	Sequence 45, Appl
25	21	87.5	334	3 US-08-873-970-45	Sequence 45, Appl
26	21	87.5	334	4 US-09-095-855-45	Sequence 45, Appl
27	21	87.5	334	4 US-08-705-347A-45	Sequence 45, Appl

28	21	87.5	334	4 US-09-324-542-45	Sequence 45, Appl
29	21	87.5	335	4 US-09-198-955A-10	Sequence 10, Appl
30	21	87.5	335	4 US-09-184-217-1	Sequence 1, Appl
31	21	87.5	340	4 US-09-188-930-184	Sequence 184, App
32	21	87.5	385	3 US-09-053-866-2	Sequence 2, Appl
33	21	87.5	389	1 US-08-409-199-3	Sequence 3, Appl
34	21	87.5	439	4 US-09-171-461-32	Sequence 32, Appl
35	21	87.5	446	3 US-08-956-254-2	Sequence 2, Appl
36	21	87.5	446	3 US-09-008-388-1	Sequence 1, Appl
37	21	87.5	448	2 US-09-015-815-1	Sequence 1, Appl
38	21	87.5	448	3 US-08-476-509B-2	Sequence 2, Appl
39	21	87.5	486	3 US-08-348-518C-2	Sequence 2, Appl
40	21	87.5	495	2 US-08-794-795-2	Sequence 2, Appl
41	21	87.5	495	4 US-09-249-200-2	Sequence 2, Appl
42	21	87.5	534	2 US-09-031-392-4	Sequence 4, Appl
43	21	87.5	534	4 US-09-299-549-4	Sequence 4, Appl
44	21	87.5	534	4 US-09-610-417-4	Sequence 4, Appl
45	21	87.5	577	4 US-09-413-814-4	Sequence 4, Appl
46	21	87.5	732	2 US-08-843-530B-28	Sequence 28, Appl
47	21	87.5	739	2 US-08-836-943-2	Sequence 2, Appl
48	21	87.5	774	2 US-08-231-193A-42	Sequence 42, Appl
49	21	87.5	774	2 US-08-486-273A-42	Sequence 42, Appl
50	21	87.5	774	3 US-08-480-474-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-176-500-41
; Sequence 41, Application US/08176500
; Patent No. 5498538
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,500
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,416
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miskoek, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 1101-143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-176-500-41

Query Match 91.7%; Score 22; DB 1; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 2
US-08-471-052A-41
; Sequence 41, Application US/08471052A
; Patent No. 5625033
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,052A
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-052A-41

Query Match 91.7%; Score 22; DB 1; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 3
US-08-189-331-41
; Sequence 41, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-41

Query Match 91.7%; Score 22; DB 1; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 4
US-08-471-939-41
; Sequence 41, Application US/08471939
; Patent No. 5844076
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,939
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,416
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-143

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-939-41

Query Match 91.7%; Score 22; DB 2; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 5
US-08-471-800-41
; Sequence 41, Application US/08471800
; Patent No. 5852167
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.

; APPLICANT: Fowkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,800
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/013,416
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-800-41

Query Match 91.7%; Score 22; DB 2; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 6
US-08-471-068-41
; Sequence 41, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.

; APPLICANT: Fowkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-068-41

Query Match 91.7%; Score 22; DB 2; Length 38;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 20 GTTSPS 25

RESULT 7
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin

; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida

; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-617-2

Query Match 91.7%; Score 22; DB 1; Length 166;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|||
Db 160 GTAAPS 165

RESULT 8
US-08-353-476-73
; Sequence 73, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-353-476-73

Query Match 91.7%; Score 22; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|||
Db 119 GTATPS 124

RESULT 9
US-08-353-476-116
; Sequence 116, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-353-476-116

Query Match 91.7%; Score 22; DB 2; Length 241;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|||
Db 192 GTATPS 197

RESULT 10

US-08-353-476-112
; Sequence 112, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-353-476-112

Query Match 91.7%; Score 22; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 224 GTATPS 229

RESULT 11
US-09-372-422A-40
; Sequence 40, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-40

Query Match 91.7%; Score 22; DB 4; Length 294;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 158 GTTTPS 163

RESULT 12
US-09-428-711A-16
; Sequence 16, Application US/09428711A
; Patent No. 6358720
; GENERAL INFORMATION:
; APPLICANT: Muramatsu, Masaaki
; APPLICANT: Shirasawa, Takuji
; APPLICANT: Tokumitsu, Hiroshi
; APPLICANT: No. 6358720uchi, Teruhisa
; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
; FILE REFERENCE: 06501-045001
; CURRENT APPLICATION NUMBER: US/09/428,711A
; CURRENT FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: PCT/JP98/01246
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: JP 9/124798
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-428-711A-16

Query Match 91.7%; Score 22; DB 4; Length 1050;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 745 GTSSPS 750

RESULT 13
PCT-US96-08730-14
; Sequence 14, Application PC/TUS9608730
; GENERAL INFORMATION:
; APPLICANT: Cassels, Frederick
; APPLICANT: Anderson, Jeffrey
; APPLICANT: Carter, John Mark
; TITLE OF INVENTION: Methods of Raising Antibodies Against E.
; TITLE OF INVENTION: Coli of the Family CSF-CFA /1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glenna Hendricks
; STREET: P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: USA
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08730
; FILING DATE: 03-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: PCT/US96/08730
TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PCT-US96-08730-14

Query Match 87.5%; Score 21; DB 5; Length 40;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 22 GTALPS 27

RESULT 14
US-08-537-400-32
Sequence 32, Application US/08537400
Patent No. 5939301
GENERAL INFORMATION:
APPLICANT: Cloned DNA Polymerases From Thermotoga
TITLE OF INVENTION: neapolitana And Mutants Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,400
FILING DATE: 02-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 09-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-537-400-32

Query Match 87.5%; Score 21; DB 2; Length 56;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 44 GTRTPS 49

RESULT 15
US-09-228-986-83
Sequence 83, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
US-09-228-986-83

Query Match 87.5%; Score 21; DB 4; Length 153;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 103 GTLSPS 108

RESULT 16
US-08-483-101-3
Sequence 3, Application US/08483101
Patent No. 5932715
GENERAL INFORMATION:
APPLICANT: Scott, June R.
APPLICANT: Froehlich, Barbara
APPLICANT: Caron, Judy
TITLE OF INVENTION: CS2 Proteins and Coding Sequences
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,101
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33878
REFERENCE/DOCKET NUMBER: 6-95
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-101-3

Query Match 87.5%; Score 21; DB 2; Length 170;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
| | | |
DB 45 GTALPS 50

RESULT 17
US-09-081-180-5
; Sequence 5, Application US/09081180
; Patent No. 6022847
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17C1
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-180-5

Query Match 87.5%; Score 21; DB 3; Length 170;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
| | | |

DB 95 GTYSPS 100

RESULT 18
US-09-040-786-5
; Sequence 5, Application US/09040786
; Patent No. 6025197
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,786
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-040-786-5

Query Match 87.5%; Score 21; DB 3; Length 170;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
| | | |
DB 95 GTYSPS 100

RESULT 19
US-08-290-979A-8
; Sequence 8, Application US/08290979A
; Patent No. 5610046
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, Albert J.H.
; APPLICANT: DE GRAFF, Leendert H.
; APPLICANT: VAN DEN BROECK, Henriette C.
; APPLICANT: VISSER, Jacob
; TITLE OF INVENTION: Cloning and Expression of Xylanase B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,979A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KATE H. MURASHIGE
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4615-0045.00
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSN FOERS WSH
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-290-979A-8

Query Match 87.5%; Score 21; DB 1; Length 225;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 99 GTFTPS 104

RESULT 20
US-08-481-956A-9
; Sequence 9, Application US/08481956A
; Patent No. 5824867
; GENERAL INFORMATION:
; APPLICANT: Coruzzi, Gloria
; APPLICANT: Oliveira, Igor
; APPLICANT: Lam, Hon-Ming
; APPLICANT: Hsieh, Ming-Hsiun
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,956A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-040
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-481-956A-9

Query Match 87.5%; Score 21; DB 2; Length 295;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 65 GTVSPS 70

RESULT 21
US-08-629-291A-9
; Sequence 9, Application US/08629291A
; Patent No. 5959174
; GENERAL INFORMATION:
; APPLICANT: Coruzzi, Gloria
; APPLICANT: Oliveira, Igor
; APPLICANT: Lam, Hon-Ming
; APPLICANT: Hsieh, Ming-Hsiun
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,291A
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-629-291A-9

Query Match 87.5%; Score 21; DB 2; Length 295;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 65 GTVSPS 70

RESULT 22
US-08-658-335B-9
; Sequence 9, Application US/08658335B
; Patent No. 5981703
; GENERAL INFORMATION:
; APPLICANT: Coruzzi, Gloria
; APPLICANT: Oliveira, Igor
; APPLICANT: Lam, Hon-Ming
; APPLICANT: Hsieh, Ming-Hsiun
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,335B
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-658-335B-9

Query Match 87.5%; Score 21; DB 2; Length 295;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 65 GTVSPS 70

RESULT 23
US-08-997-080-45
; Sequence 45, Application US/08997080
; Patent No. 598524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-997-080-45

Query Match 87.5%; Score 21; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 253 GTCTPS 258

RESULT 24
US-08-997-362-45
; Sequence 45, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyma, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-997-362-45

Query Match      87.5%; Score 21; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
   ||||
Db 253 GTGTPS 258

RESULT 25
US-08-873-970-45
; Sequence 45, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiwama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-855-45

Query Match      87.5%; Score 21; DB 4; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
   ||||
Db 253 GTGTPS 258

; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-873-970-45

Query Match      87.5%; Score 21; DB 3; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
   ||||
Db 253 GTGTPS 258

RESULT 26
US-09-095-855-45
; Sequence 45, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT AND DIAGNOSIS OF Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-855-45

Query Match      87.5%; Score 21; DB 4; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
   ||||
Db 253 GTGTPS 258
```

```
RESULT 27
US-08-705-347A-45
; Sequence 45, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565
; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-705-347A-45

Query Match 87.5%; Score 21; DB 4; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|||
Db 253 GTGTPS 258

RESULT 28
US-09-324-542-45
; Sequence 45, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-45

Query Match 87.5%; Score 21; DB 4; Length 334;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|||
Db 253 GTGTPS 258

RESULT 29
US-09-198-955A-10
; Sequence 10, Application US/09198955A
; Patent No. 6187580
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels E.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Moller, Soren
; APPLICANT: Glad, Sanne O. S.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Schnorr, Kirk
; APPLICANT: Kongsbak, Lars
; FILE OF INVENTION: NO. 6187580el pectate Lyases
; FILE REFERENCE: 5378.200-US
; CURRENT APPLICATION NUMBER: US/09/198,955A
; CURRENT FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1343/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,249
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 09/073,684
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/184,217
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-198-955A-10

Query Match 87.5%; Score 21; DB 4; Length 335;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|||
Db 84 GTITPS 89

RESULT 30
US-09-184-217-1
; Sequence 1, Application US/09184217
; Patent No. 6258590
; GENERAL INFORMATION:
; APPLICANT: Lange, Niels E.K.
; APPLICANT: Kongsbak, Lars
; APPLICANT: Schulein, Martin
```

; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Husain, Philip A.
; TITLE OF INVENTION: Biopreparation Of Textiles At High
; TITLE OF INVENTION: Temperatures
; FILE REFERENCE: 5729.000-US
; CURRENT APPLICATION NUMBER: US/09/184,217
; CURRENT FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 335
; TYPE: PRT
; ORGANISM: bacillus sp.
US-09-184-217-1

Query Match 87.5%; Score 21; DB 4; Length 335;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 84 GTTPS 89

RESULT 31
US-09-188-930-184
; Sequence 184, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 184
; LENGTH: 340
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-184

Query Match 87.5%; Score 21; DB 4; Length 340;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 120 GTAGPS 125

RESULT 32
US-09-053-866-2
; Sequence 2, Application US/09053866
; Patent No. 611075
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Presnell, Scott R.
; APPLICANT: Yee, David P.
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
; TITLE OF INVENTION: PAR4 (ZCHEMR2)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East

; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leith, Debra K
; REGISTRATION NUMBER: 32,619
; REFERENCE/DOCKET NUMBER: 98-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6674
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-053-866-2

Query Match 87.5%; Score 21; DB 3; Length 385;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 19 GTQTPS 24

RESULT 33
US-08-409-199-3
; Sequence 3, Application US/08409199
; Patent No. 5532153
; GENERAL INFORMATION:
; APPLICANT: XU, Shuang-yong
; APPLICANT: XIAO, Jianping
; TITLE OF INVENTION: METHOD FOR CLONING AND
; TITLE OF INVENTION: PRODUCING THE Sact RESTRICTION
; TITLE OF INVENTION: ENDONUCLEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,199
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.

; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054; 292
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-409-199-3

Query Match 87.5%; Score 21; DB 1; Length 389;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 375 GTTIPS 380

RESULT 34
US-09-171-461-32
; Sequence 32, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chiocca, Susanna
; APPLICANT: Kurzbaumer, Robert
; APPLICANT: Schafner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; EARLIER FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; EARLIER FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 439
; TYPE: PRT
; ORGANISM: CELO VIRUS
; FEATURE:
; OTHER INFORMATION: Position: 5366..6685/Product.IVa2
US-09-171-461-32

Query Match 87.5%; Score 21; DB 4; Length 439;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 19 GTKTPS 24

RESULT 35
US-08-956-254-2
; Sequence 2, Application US/08956254A
; Patent No. 6013265
; GENERAL INFORMATION:
; APPLICANT: AURELIAN, LAURE
; TITLE OF INVENTION: Vaccine Composition for Herpes Simplex Virus and
; TITLE OF INVENTION: Methods of Using
; FILE REFERENCE: 1421LA
; CURRENT APPLICATION NUMBER: US/08/956,254A
; CURRENT FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/029,093
; EARLIER FILING DATE: 1996-10-22
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 446
; TYPE: PRT
; ORGANISM: herpes simplex virus-2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(446)
; OTHER INFORMATION: PROTEIN KINASE DOMAIN OF ICP10 SUBUNIT OF HSV-2
; PUBLICATION INFORMATION:
; AUTHORS: CHUNG ET AL.,
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 3389-3398
; DATE: 1989
; PUBLICATION INFORMATION:
; AUTHORS: NELSON ET AL.,
; JOURNAL: J. Biol. Chem.
; VOLUME: 271
; PAGES: 17021-17027
; DATE: 1996
US-08-956-254-2

Query Match 87.5%; Score 21; DB 3; Length 446;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 116 GTSGPS 121

RESULT 36
US-09-008-388-1
; Sequence 1, Application US/09008388
; Patent No. 6054131
; GENERAL INFORMATION:
; APPLICANT: AURELIAN, LAURE
; TITLE OF INVENTION: VACCINE COMPOSITION FOR HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS AND METHOD OF USING
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PEPPER HAMILTON LLP
; STREET: 600 FOURTEENTH STREET, N.W., Suite 500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005-2004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-WINDOWS
; SOFTWARE: WP 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,388
; FILING DATE: December 2, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramsey, William S.
; REGISTRATION NUMBER: 32,715
; REFERENCE/DOCKET NUMBER: 114178.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 220-1280
; TELEFAX: (202) 220-1665
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE:
ORGANISM: HERPES SIMPLEX
STRAIN: RECOMBINANT
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-008-388-1

Query Match 87.5%; Score 21; DB 3; Length 446;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 116 GTSGPS 121

RESULT 37

US-09-015-815-1
Sequence 1, Application US/09015815
Patent No. 5965356
GENERAL INFORMATION:
APPLICANT: AURELIAN, LAURE
APPLICANT: SMITH, CYNTHIA
TITLE OF INVENTION: HERPES SIMPLEX VIRUS TYPE SPECIFIC SEROASSAY
FILE REFERENCE: 1437LA
CURRENT APPLICATION NUMBER: US/09/015,815
CURRENT FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: US 60/036,622
EARLIER FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 448
TYPE: PRT
ORGANISM: herpes simplex virus-2
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(446)
OTHER INFORMATION: PROTEIN KINASE DOMAIN OF ICP10 SUBUNIT OF HSV-2
PUBLICATION INFORMATION:
AUTHORS: CHUNG ET AL.,
JOURNAL: J. Virol.,
VOLUME: 63
PAGES: 3389-3398
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: NELSON ET AL.,
JOURNAL: J. Biol. Chem.,
VOLUME: 271
PAGES: 17021-17027
DATE: 1996
US-09-015-815-1

Query Match 87.5%; Score 21; DB 2; Length 448;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 116 GTSGPS 121

RESULT 38

US-08-476-509B-2
Sequence 2, Application US/08476509B
Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-509B-2

Query Match 87.5%; Score 21; DB 3; Length 448;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 139 GTLTPS 144

RESULT 39

US-08-348-518C-2
Sequence 2, Application US/08348518C
Patent No. 6022740
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A

;; TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
;; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
;; TITLE OF INVENTION: THEREOF
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/348,518C
;; FILING DATE: 01-DEC-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 486 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-348-518C-2

Query Match 87.5%; Score 21; DB 3; Length 486;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 139 GTLTPS 144

RESULT 40
US-08-794-795-2
;; Sequence 2, Application US/08794795
;; Patent No. 5916766
;; GENERAL INFORMATION:
;; APPLICANT: Elshourlagy, Nabil
;; APPLICANT: Adamou, John
;; APPLICANT: Gross, Mitchell
;; APPLICANT: Lysko, Paul
;; TITLE OF INVENTION: Human Macro Scavenger Rec
;; TITLE OF INVENTION: eptor
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/794,795
;; FILING DATE: 04-FEB-1997

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: ATG50009P
;; FILING DATE: 22-MAY-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Han, William T
;; REGISTRATION NUMBER: 34,344
;; REFERENCE/DOCKET NUMBER: ATG500009
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5219
;; TELEFAX: 610-270-4026
;; TELEX:
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 495 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-794-795-2

Query Match 87.5%; Score 21; DB 2; Length 495;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 162 GTTGPS 167

RESULT 41
US-09-249-200-2
;; Sequence 2, Application US/09249200
;; Patent No. 6197931
;; GENERAL INFORMATION:
;; APPLICANT: ELSHOURBAGY, NABIL
;; APPLICANT: ADAMOU, JOHN
;; APPLICANT: GROSS, MITCHELL
;; APPLICANT: LYSKO, PAUL
;; TITLE OF INVENTION: HUMAN MARCO SCAVENGER RECEPTOR
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ratner & Prestia
;; STREET: P.O. Box 980
;; CITY: Valley Forge
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19482
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/249,200
;; FILING DATE: 12-FEB-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/794,795
;; FILING DATE: 04-FEB-1997
;; APPLICATION NUMBER: 60/017,699
;; FILING DATE: 23-MAY-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Prestia, Paul F
;; REGISTRATION NUMBER: 23,031
;; REFERENCE/DOCKET NUMBER: ATG-50009-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-407-0700
;; TELEFAX: 610-407-0700
;; TELEX: 846169
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:

; LENGTH: 495 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-249-200-2

Query Match 87.5%; Score 21; DB 4; Length 495;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 162 GTTGPS 167

RESULT 42
US-09-031-392-4
; Sequence 4, Application US/09031392
; Patent No. 5942398
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Weng, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-392-4

Query Match 87.5%; Score 21; DB 2; Length 534;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 87 GTLAPS 92

RESULT 43
US-09-299-549-4
; Sequence 4, Application US/09299549
; Patent No. 6136547
; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Weng, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,549
; FILING DATE: 26-APR-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-549-4

Query Match 87.5%; Score 21; DB 4; Length 534;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 87 GTLAPS 92

RESULT 44
US-09-610-417-4
; Sequence 4, Application US/09610417
; Patent No. 6346374
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Weng, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,417

; FILING DATE: 05-Jul-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/299,549
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Melklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-610-417-4

Query Match 87.5%; Score 21; DB 4; Length 534;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 87 GTLAPS 92

RESULT 45
US-09-413-814-4
; Sequence 4; Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bloeker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
; FILE REFERENCE: PCT/US 99/23535
; CURRENT APPLICATION NUMBER: US/09/413,814
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-4

Query Match 87.5%; Score 21; DB 4; Length 577;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 371 GTALPS 376

RESULT 46

US-08-843-530B-28
; Sequence 28; Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-843-530B-28

Query Match 87.5%; Score 21; DB 2; Length 732;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 81 GTLSPS 86

RESULT 47
US-08-836-943-2
; Sequence 2; Application US/08836943
; Patent No. 5965391
; GENERAL INFORMATION:
; APPLICANT: Reinscheid, Dieter
; APPLICANT: Eikmanns, Bernhard
; APPLICANT: Sahm, Hermann
; TITLE OF INVENTION: DNA WHICH REGULATES GENE EXPRESSION IN
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Firm of Karl F. Ross, PC
; STREET: 5676 Riverdale Ave.
; CITY: Bronx
; STATE: New York
; COUNTRY: USA
; ZIP: 10471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,943
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Jonathan
; REGISTRATION NUMBER: 26,963
; REFERENCE/DOCKET NUMBER: 20357
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (718) 884-6600
; TELEFAX: 718/601-1099
; TELEX: 620428
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 739 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-943-2

Query Match 87.5%; Score 21; DB 2; Length 739;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 716 GTKSPS 721

RESULT 48
US-08-231-193A-42
; Sequence 42, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 774 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-231-193A-42

Query Match 87.5%; Score 21; DB 2; Length 774;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 292 GTVSPS 297

RESULT 49
US-08-486-273A-42
; Sequence 42, Application US/08486273A
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-273A-42

Query Match 87.5%; Score 21; DB 2; Length 774;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 292 GTVSPS 297

RESULT 50
US-08-480-474-42
; Sequence 42, Application US/08480474
; Patent No. 6033865
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
; TITLE OF INVENTION: SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,474
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9382B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-474-42

Query Match 87.5%; Score 21; DB 3; Length 774;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|||
Db 292 GTVSPS 297

Search completed: September 3, 2002, 09:25:31
Job time: 23 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2002, 09:25:08 ; Search time 14.73 Seconds
(without alignments)
39.140 Million cell updates/sec

Title: BASK-853-CLAIM5
Perfect score: 24
Sequence: 1 gtxxps 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	22	91.7	89	2	B31141
2	22	91.7	101	2	S30493
3	22	91.7	105	2	G72515
4	22	91.7	111	2	A85695
5	22	91.7	135	2	JC2424
6	22	91.7	194	2	H90836
7	22	91.7	196	2	I39698
8	22	91.7	196	2	T51838
9	22	91.7	202	2	B82133
10	22	91.7	254	2	A83345
11	22	91.7	255	2	E42725
12	22	91.7	275	2	S47325
13	22	91.7	280	2	H71320
14	22	91.7	285	2	H85356
15	22	91.7	289	2	T17957
16	22	91.7	316	2	T34553
17	22	91.7	319	2	S62196
18	22	91.7	379	2	JN0013
19	22	91.7	381	2	S12223
20	22	91.7	383	2	E87549
21	22	91.7	389	1	SPJCU
22	22	91.7	389	2	JC5136
23	22	91.7	398	2	S42523
24	22	91.7	410	2	S12224
25	22	91.7	418	2	F75587
26	22	91.7	419	1	SVJCD
27	22	91.7	419	2	T36272
28	22	91.7	421	2	T41156
29	22	91.7	435	2	T24477

30	22	91.7	460	2	S34969	outer membrane por
31	22	91.7	460	2	T23087	hypothetical prote
32	22	91.7	507	2	T26809	hypothetical prote
33	22	91.7	518	2	F75460	hypothetical prote
34	22	91.7	522	2	T40520	hypothetical prote
35	22	91.7	542	2	T48488	hypothetical prote
36	22	91.7	550	2	B70583	probable transposa
37	22	91.7	574	2	T29005	hypothetical prote
38	22	91.7	593	2	A96783	unknown protein F2
39	22	91.7	597	2	T35746	hypothetical prote
40	22	91.7	629	2	S20516	dnaK-type molecula
41	22	91.7	651	2	A96781	unknown protein F9
42	22	91.7	691	2	B75622	hypothetical prote
43	22	91.7	693	2	T15152	hypothetical prote
44	22	91.7	696	2	A29635	transcription fact
45	22	91.7	756	2	D96527	protein F27J15.24
46	22	91.7	788	2	J50747	regulatory protein
47	22	91.7	848	2	T28055	hypothetical prote
48	22	91.7	875	2	T20429	hypothetical prote
49	22	91.7	886	1	A47521	capsid protein - g
50	22	91.7	963	2	T40290	hypothetical prote

ALIGNMENTS

RESULT 1

E83141
hypothetical protein PA0033 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83141
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: A82950; MUID:20437337
A:Accession: E83141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: GB:AE004820; GB:AE004091; NID:g9950223; PIDN:AAG07420.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0033

Query Match 91.7%; Score 22; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
|| ||
Db 48 GTASPS 53

RESULT 2

S30493
Spi protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S30493
R:Chestier, A.; Charnay, P.
DNA Seq. 2, 325-327, 1992
A:Title: Difference in the genomic organizations of the related transcription factors naringenin-chalcon and naringenin-chalcon.
A:Reference number: S30493; MUID:92338398
A:Accession: S30493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <CHE>
A:Cross-references: EMBL:X60136; NID:954158; PIDN:CAA42721.1; PID:e38120; PID:g133426

Query Match 91.7%; Score 22; DB 2; Length 101;
 Best Local Similarity 66.7%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 Db 52 GTATPS 57

RESULT 3
 G72515
 hypothetical protein APE2100 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: G72515
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A:Reference number: A72450; MUID:99310339
 A:Accession: G72515
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-105 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81111.1; PID:dl044897; PID:g510
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2100

Query Match 91.7%; Score 22; DB 2; Length 105;
 Best Local Similarity 66.7%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 Db 15 GTSSPS 20

RESULT 4
 A85695
 hypothetical protein Z1932 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85695
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85695
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-111 <STO>
 A:Cross-references: GB:AE005174; NID:gl2514864; PIDN:AAG56021.1; GSPDB:GN00145; UWGP:Z19
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z1932

Query Match 91.7%; Score 22; DB 2; Length 111;
 Best Local Similarity 66.7%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 Db 55 GTSSPS 60

RESULT 5
 JC2424
 hypothetical 14.3K protein - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 01-Feb-1995 #sequence_revision 26-May-1995 #text_change 26-May-1995
 C:Accession: JC2424
 R:Harada, T.; Saito, H.; Kouhara, H.; Kurebayashi, S.; Kasayama, S.; Terakawa, N.; Ki
 Biochem. Biophys. Res. Commun. 205, 1057-1063, 1994
 A:Title: Murine fibroblast growth factor receptor 1 gene generates multiple messenger
 A:Reference number: FC2277; MUID:95100926
 A:Accession: JC2424
 A:Molecule type: DNA
 A:Residues: 1-135 <HAR>
 A:Note: The authors translated the codon CAG for residue 113 as Glu and AAC for resid

Query Match 91.7%; Score 22; DB 2; Length 135;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 Db 105 GTAAPS 110

RESULT 6
 H90836
 hypothetical protein ECS1664 [imported] - Escherichia coli (strain O157:H7, substrain
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: H90836
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: H90836
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-194 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA035087.1; PID:gl3361128; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECS1664

Query Match 91.7%; Score 22; DB 2; Length 194;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 Db 49 GTSSPS 54

RESULT 7
 I39698
 blue copper-binding protein, 20K - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 11-Jun-1999
 C:Accession: I39698; S25555
 R:Van Gysel, A.; Van Montagu, M.; Inze, D.
 Gene 136, 79-85, 1993
 A:Title: A negatively light-regulated gene from Arabidopsis thaliana encodes a protei
 A:Reference number: I39698; MUID:94124044
 A:Accession: I39698
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-196 <RES>
 A:Cross-references: EMBL:Z15058; NID:gl6202; PIDN:CAA78771.1; PID:gl6203
 C:Genetics:
 A:Gene: bcb

A:Introns: 57/3
 C:Superfamily: plastocyanin
 C:Keywords: copper binding; transmembrane protein
 F:66,107,112,117/Binding site: copper (His, Cys, His, Gln) #status predicted

F:79-113/Disulfide bonds: #status predicted

Query Match 91.7% Score 22; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 158 GTTTPS 163

RESULT 8

T51838
blue copper binding protein homolog [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000

C:Accession: T51838

R:Yang, K.Y.; Kim, C.S.; Cho, B.H.

submitted to the EMBL Data Library, October 1998

A:Description: Characterization of a wound-inducible Arabidopsis gene encoding a protein

A:Reference number: Z25481

A:Accession: T51838

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-196 <YAN>

A:Cross-references: EMBL:Y18227; PIDN:CAA77089.1

C:Genetics:

A:Gene: AWI 32

C:Superfamily: plastocyanin

C:Keywords: copper binding

Query Match 91.7% Score 22; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 158 GTTTPS 163

RESULT 9

B82133
probable outer membrane lipoprotein Slp VC1987 [imported] - Vibrio cholerae (strain N169

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 23-Mar-2001

C:Accession: B82133

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833

A:Accession: B82133

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-202 <HEI>

A:Cross-references: GB:AE004273; GB:AE003852; NID:9656517; PIDN:AAF95135.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1987

A:Map position: 1

C:Superfamily: rnd protein

Query Match 91.7% Score 22; DB 2; Length 202;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 134 GTTAPS 139

RESULT 10

A83345

Probable thioesterase PA2411 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83345

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: A83345

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-254 <STO>

A:Cross-references: GB:AE004668; GB:AE004091; NID:g9948446; PIDN:AAG05799.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2411

C:Superfamily: oleoyl-[acyl-carrier-protein] hydrolase; oleoyl-[acyl-carrier-protein]

Query Match 91.7% Score 22; DB 2; Length 254;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 108 GTTAPS 113

RESULT 11

E42725

nitrite hydratase 3'-hypothetical protein orfE - Pseudomonas chlororaphis (strain B23

C:Species: Pseudomonas chlororaphis

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999

C:Accession: E42725

R:Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.

J. Bacteriol. 173, 2465-2472, 1991

A:Title: Cloning and characterization of genes responsible for metabolism of nitrile

A:Reference number: A42725; MUID:91193202

A:Accession: E42725

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-255 <NIS>

A:Cross-references: GB:D90216; NID:g216850; PIDN:BAA14248.1; PID:d1014953; PID:g21602

Query Match 91.7% Score 22; DB 2; Length 255;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 103 GTTAPS 108

RESULT 12

S47325

myoD protein - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Dec-2000

C:Accession: S47325

R:Weinberg, E.S.

submitted to the EMBL Data Library, September 1994

A:Description: Developmental regulation of zebrafish myo D in wild type, no tail, and

A:Reference number: S47325

A:Accession: S47325

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-275 <WEI>
 A;Cross-references: EMBL:Z36945; NID:g535814; PID:g535815
 C;Superfamily: human myogenin

Query Match 91.7%; Score 22; DB 2; Length 275;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 253 GTTAPS 258

RESULT 13

H71320
 hypothetical protein TP0462 - syphilis spirochete
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C;Accession: H71320
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; MUID:98332770
 A;Accession: H71320
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-280 <COL>
 A;Cross-references: GB:AF001223; GB:AE000520; NID:g3322745; PID:g332275
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0462

Query Match 91.7%; Score 22; DB 2; Length 280;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 116 GTTTPS 121

RESULT 14

H85356
 hypothetical protein AT4g30510 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C;Accession: H85356
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488
 A;Accession: H85356
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-285 <STO>
 A;Cross-references: GB:NC_001268; NID:g7269952; PIDN:CAB79769.1; GSPDB:GN00140
 C;Genetics:
 A;Gene: AT4g30510
 A;Map position: 4

Query Match 91.7%; Score 22; DB 2; Length 285;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 233 GTSSPS 238

RESULT 15

TI7957
 hypothetical protein A454L - Chlorella virus PBCV-1
 C;Species: Chlorella virus PBCV-1
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C;Accession: TI7957
 R;Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A;Reference number: Z18806
 A;Accession: TI7957
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-289 <GRA>
 A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96822.1
 A;Experimental source: specific host Chlorella strain NC64
 C;Genetics:
 A;Note: A454L
 C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A454L

Query Match 91.7%; Score 22; DB 2; Length 289;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 271 GTATPS 276

RESULT 16

T34553
 hypothetical protein DKF2p434L1435.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 03-Nov-2000
 C;Accession: T34553
 R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, October 1999
 A;Reference number: Z21540
 A;Accession: T34553
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-316 <POU>
 A;Cross-references: EMBL:AL122037
 A;Experimental source: adult testis; clone DKF2p434L1435
 C;Genetics:
 A;Note: DKF2p434L1435.1
 C;Superfamily: valine--tRNA ligase

Query Match 91.7%; Score 22; DB 2; Length 316;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 217 GTAAPS 222

RESULT 17

S62196
 hypothetical protein 2 - Methanosarcina barkeri
 C;Species: Methanosarcina barkeri
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Oct-1999
 C;Accession: S62196
 R;Vorholt, J.A.; Vaupel, M.; Thauer, R.K.
 Eur. J. Biochem. 236, 309-317, 1996
 A;Title: A polyferredoxin with eight [4Fe-4S] clusters as a subunit of molybdenum for
 A;Reference number: S62194; MUID:96184912
 A;Accession: S62196
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-319 <VOR>

A:Cross-references: EMBL:X93084; NID: g1124956; PIDN:CAA63627.1; PID: g1124956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

Query Match 91.7%; Score 22; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 2.3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 gtxxps 6
|| ||
Db 66 GTSSPS 71

RESULT 18

JN0013

Synaptic vesicle membrane protein VAT-1 - Pacific electric ray

C:Species: Torpedo californica (Pacific electric ray)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Mar-2000

C:Accession: JN0013

R:Linial, M.; Miller, K.; Scheller, R.H.

Neuron 2, 1265-1273, 1989

A:Title: VAT-1: an abundant membrane protein from torpedo cholinergic synaptic vesicles.

A:Reference number: JN0013; MUID:90166593

A:Accession: JN0013

A:Molecule type: mRNA

A:Residues: 1-379 <LIN>

C:Comment: Synaptic vesicles are responsible for regulating the storage and release of n

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: glycoprotein; membrane protein; phosphoprotein

F:52-350/Domain: long-chain alcohol dehydrogenase homology <LADH>

F:67,127,147/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:273/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 91.7%; Score 22; DB 2; Length 379;
Best Local Similarity 66.7%; Pred. No. 2.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 gtxxps 6
|| ||
Db 194 GRATSPS 199

RESULT 19

S12223

naringenin-chalcone synthase (EC 2.3.1.74) 1 - tomato

C:Species: Lycopersicon esculentum {tomato}

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-May-2000

C:Accession: S12223

R:O'Neill, S.D.; Tong, Y.; Spoerlein, B.; Forkmann, G.; Yoder, J.I.

Mol. Gen. Genet. 224, 279-288, 1990

A:Title: Molecular genetic analysis of chalcone synthase in Lycopersicon esculentum and

A:Reference number: S12223; MUID:91117196

A:Accession: S12223

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-381 <ONE>

C:Genetics:

A:Map position: 9

C:Superfamily: chalcone synthase

C:Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 91.7%; Score 22; DB 2; Length 381;
Best Local Similarity 66.7%; Pred. No. 2.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 gtxxps 6
|| ||
Db 23 GTSTPS 28

RESULT 20

JC5136

naringenin-chalcone synthase (EC 2.3.1.74) 2 - potato

N:Alternate names: chalcone synthase; CHS

C:Species: Solanum tuberosum (potato)

E87549

Type IV secretion system protein B10, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: E87549

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; K

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87549

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-383 <STO>

A:Cross-references: GB:AE005673; NID: g13423963; PIDN:AAK24393.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2422

C:Superfamily: tumor-inducing plasmid pTic58 virB10 protein

Query Match 91.7%; Score 22; DB 2; Length 383;
Best Local Similarity 66.7%; Pred. No. 2.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 gtxxps 6
|| ||
Db 74 GRATSPS 79

RESULT 21

SYPJCJ

naringenin-chalcone synthase (EC 2.3.1.74) J - garden petunia

N:Alternate names: chalcone synthase

C:Species: Petunia x hybrida (garden petunia)

C:Date: 30-Sep-1991 #sequence_revision 17-Mar-2000 #text_change 05-May-2000

C:Accession: D72821; JS0309

R:Koes, R.E.; Spelt, C.E.; van den Elzen, P.J.M.; Mol, J.N.M.

Gene 81, 245-257, 1989

A:Title: Cloning and molecular characterization of the chalcone synthase multigene fa

A:Reference number: JS0308; MUID:90034197

A:Accession: D72821

A:Molecule type: DNA

A:Residues: 1-389 <KOE>

A:Cross-references: EMBL:X14597; NID: g20535; PIDN:CAA32737.1; PID: g20536

A:Experimental source: strain Violet 30, leaf

A:Accession: JS0309

A:Molecule type: DNA

A:Residues: 1-50, 'D', 52-74, 'V', 76-228, 'I', 230-297, 'L', 299-389 <KO2>

A:Note: the sequence is revised in GenBank entry PHCHSJ release 114, (PIDN:CAA32737.1

C:Comment: This enzyme plays a central role in the biosynthesis of all classes of fla

C:Genetics:

A:Gene: chsJ

A:Map position: V

A:Note: chsJ is expressed in various floral tissues and UV illuminated seedlings

C:Superfamily: chalcone synthase

C:Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 91.7%; Score 22; DB 1; Length 389;
Best Local Similarity 66.7%; Pred. No. 2.8e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 gtxxps 6
|| ||
Db 23 GRATPS 28

C;Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 05-May-2000

C;Accession: JC5136; PC4239

R;Jeon, J.H.; Kim, H.S.; Choi, K.H.; Joung, Y.H.; Joung, H.; Byun, S.M.

Biosci. Biotechnol. Biochem. 60, 1907-1910, 1996

A;Title: Cloning and characterization of one member of the chalcone synthase gene family

A;Reference number: JC5136; MUID:97141614

A;Accession: JC5136

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-389 <JEO1>

A;Cross-references: GB:U47738; NID:g1470059; PIDN:AB05239.1; PID:g1470060

A;Accession: PC4239

A;Status: preliminary

A;Molecule type: protein

A;Residues: 158-165;367-373 <JEO2>

C;Comment: This enzyme is important in the biosynthesis of all classes of flavonoids in

C;Superfamily: chalcone synthase

C;Keywords: acyltransferase; coenzyme A

Query Match 91.7%; Score 22; DB 2; Length 389;

Best Local Similarity 66.7%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 23 GTATPS 28

RESULT 23

S42523

naringenin-chalcone synthase (EC 2.3.1.74) - parsley

N;Alternate names: chalcone synthase

C;Species: Petroselinum crispum (parsley)

C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C;Accession: S42523

R;Reimold, U.; Kroeger, M.; Kreuzaler, F.; Hahlbrock, K.

EMBO J. 2, 1801-1805, 1983

A;Title: Coding and 3' non-coding nucleotide sequence of chalcone synthase mRNA and ass

A;Reference number: S42523

A;Accession: S42523

A;Molecule type: mRNA

A;Residues: 1-398 <REI>

A;Cross-references: EMBL:V01538; NID:g20513; PIDN:CAA24779.1; PID:g20514

A;Note: the source is designated as Petroselinum hortense

C;Superfamily: chalcone synthase

C;Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 91.7%; Score 22; DB 2; Length 398;

Best Local Similarity 66.7%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 28 GTATPS 33

RESULT 24

S12224

naringenin-chalcone synthase (EC 2.3.1.74) 2 - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-May-2000

C;Accession: S12224

R;O'Neill, S.D.; Tong, Y.; Spoerlein, B.; Forkmann, G.; Yoder, J.I.

Mol. Gen. Genet. 224, 279-288, 1990

A;Title: Molecular genetic analysis of chalcone synthase in Lycopersicon esculentum and

A;Reference number: S12223; MUID:91117196

A;Accession: S12224

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-410 <ONE>

C;Genetics:

A;Map position: 5

C;Superfamily: chalcone synthase

C;Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 91.7%; Score 22; DB 2; Length 410;

Best Local Similarity 66.7%; Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 23 GTATPS 28

RESULT 25

F75587

probable glycosyltransferase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C;Accession: F75587

R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896

A;Accession: F75587

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-418 <WHI>

A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12451.1; PID:g646

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRA0329

A;Map position: 2

C;Superfamily: glycosyltransferase

Query Match 91.7%; Score 22; DB 2; Length 418;

Best Local Similarity 66.7%; Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 365 GTATPS 370

RESULT 26

SYPUCD

naringenin-chalcone synthase (EC 2.3.1.74) D - garden petunia

N;Alternate names: chalcone synthase

C;Species: Petunia x hybrida (garden petunia)

C;Date: 30-Sep-1991 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000

C;Accession: A72821; JS0312

R;Koes, R.E.; Spelt, C.E.; van den Elzen, P.J.M.; Mol, J.N.M.

Gene 81, 245-257, 1989

A;Title: Cloning and molecular characterization of the chalcone synthase multigene fa

A;Reference number: JS0308; MUID:90034197

A;Accession: A72821

A;Molecule type: DNA

A;Residues: 1-419 <ROE>

A;Cross-references: GB:X14593; NID:g20528; PIDN:CAA32733.1; PID:g20529

A;Experimental source: strain Violet 30, leaf

A;Accession: JS0312

A;Molecule type: DNA

A;Residues: 1-117,'D',119,'H',121-313,'DI',316-419 <KO2>

A;Note: the sequence was revised in GenBank entry PHCHSD, release 114, (PIDN:CAA32733

C;Comment: This enzyme plays a central role in the biosynthesis of all classes of fla

C;Genetics:

A;Gene: chsd

A;Map position: V

C;Superfamily: chalcone synthase

C;Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

```

Query Match          91.7%; Score 22; DB 1; Length 419;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 23 GTATPS 28

RESULT 27
T36272
hypothetical protein SCE68.22 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36272
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21576
A:Accession: T36272
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-419 <MUR>
A:Cross-references: EMBL:AL079345; PIDN:CAB45358.1; GSPDB:GN00070; SCODEB:SCE68.22
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SCE68.22

Query Match          91.7%; Score 22; DB 2; Length 419;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 380 GRASPS 385

RESULT 28
T41156
probable WD repeat transcription regulation protein - fission yeast (Schizosaccharomyces
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C:Accession: T41156
R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21973
A:Accession: T41156
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-421 <HIL>
A:Cross-references: EMBL:AL031907; PIDN:CAA21427.1; GSPDB:GN00068; SPDB:SPCC18.13
A:Experimental source: strain 972h-; cosmid c18
C:Genetics:
A:Gene: SPDB:SPCC18.13
A:Map position: 3
A:Introns: 227/2

Query Match          91.7%; Score 22; DB 2; Length 421;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 410 GRSSPS 415

RESULT 29
T24477
hypothetical protein T04H1.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T24477
R:Harris, B.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19896
A:Accession: T24477
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-435 <WIL>
A:Cross-references: EMBL:Z78200; PIDN:CAB01584.1; GSPDB:GN00023; CESP:T04H1.7
A:Experimental source: clone T04H1
C:Genetics:
A:Gene: CESP:T04H1.7
A:Map position: 5
A:Introns: 54/3; 82/3; 193/1; 239/3; 282/3; 360/1
C:Superfamily: glucuronosyltransferase

Query Match          91.7%; Score 22; DB 2; Length 435;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 300 GTTTPS 305

RESULT 30
S34969
outer membrane porin OprE precursor PA0291 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Jun-2001
C:Accession: S34969; E83608
R:Yamano, Y.; Nishikawa, T.; Komatsu, Y.
Mol. Microbiol. 8, 993-1004, 1993
A:Title: Cloning and nucleotide sequence of anaerobically induced porin protein El (O
A:Reference number: S34969; MUID:93360827
A:Accession: S34969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <YAM>
A:Cross-references: GB:D12711; NID:g433417; PIDN:BAA02207.1; PID:g433418
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: E83608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <STO>
A:Cross-references: GB:AE004467; GB:AE004091; NID:g9946133; PIDN:AAG03680.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: OprE; PA0291
C:Superfamily: Pseudomonas aeruginosa outer membrane porin PA0958

Query Match          91.7%; Score 22; DB 2; Length 460;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 54 GTASPS 59

RESULT 31
T23087
hypothetical protein H13N06.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

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C:Accession: T23087

R:Renard, N.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19673

A:Accession: T23087

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-460 <WIL>

A:Cross-references: EMBL:Z99942; PIDN:CAB17068.1; GSPDB:GN00028; CESP:H13N06.2

A:Experimental source: clone H13N06

C:Genetics:

A:Gene: CESP:H13N06.2

A:Map position: X

A:Introns: 17/1; 294/1; 331/3; 364/1; 414/2; 432/2

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 460;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 86 GTSTPS 91

RESULT 32

T26809.

hypothetical protein Y66A7A.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T26809; T27293

R:Steward, C.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z20269

A:Accession: T26809

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-507 <WIL>

A:Cross-references: EMBL:AL032627; PIDN:CAA21552.1; CESP:Y66A7A.8

A:Experimental source: clone Y41C4A

R:Matthews, L.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z20338

A:Accession: T27293

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-507 <WT2>

A:Cross-references: EMBL:AL032622; PIDN:CAA21503.1; GSPDB:GN00021; CESP:Y66A7A.8

A:Experimental source: clone Y66A7A

C:Genetics:

A:Gene: CESP:Y66A7A.8

A:Map position: 3

A:Introns: 29/3; 93/1; 145/2; 314/3; 358/3

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 507;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 425 GTSSPS 430

RESULT 33

F75460

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: F75460

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: F75460

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-518 <WHI>

A:Cross-references: GB:AE001943; GB:AE000513; NID:G6458624; PIDN:AAF10486.1; PID:G645

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0903

A:Map position: 1

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 518;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 179 GTTTPS 184

RESULT 34

T40520

hypothetical protein SPBC530.04 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40520

R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z21934

A:Accession: T40520

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-522 <LYN>

A:Cross-references: EMBL:AL023634; PIDN:CAA19170.1; GSPDB:GN00067; SPDB:SPBC530.04

A:Experimental source: strain 972h-; cosmid c530

C:Genetics:

A:Gene: SPDB:SPBC530.04

A:Map position: 2

A:Introns: 20/3

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 522;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 41 GTSAPS 46

RESULT 35

T48488

hypothetical protein T28J14.110 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T48488

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24493

A:Accession: T48488

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-542 <BEV>

A:Cross-references: EMBL:AL163652

A:Experimental source: cultivar Columbia; BAC clone T28J14

C:Genetics:

A:Map position: 5

A:Introns: 162/3; 227/1; 251/1; 299/2; 355/3; 377/2; 397/3; 419/3; 435/3; 449/2; 487/

A:Note: T28J14.110

Query Match 91.7%; Score 22; DB 2; Length 542;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 400 GTTSPS 405

RESULT 36
B70583
Probable transposase for IS1535 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: B70583
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: B70583
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-550 <COL>
A:Cross-references: GB:J95210; GB:AL123456; NID:g3261757; PIDN:CAB08504.1; PID:e315222;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0922

Query Match 91.7%; Score 22; DB 2; Length 550;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 497 GTTAPS 502

RESULT 37
T29005
Hypothetical protein ZK328.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29005
R:Favellio, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid ZK328.
A:Reference number: Z20552
A:Accession: T29005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-574 <FAV>
A:Cross-references: EMBL:U50193; PIDN:AAA91246.1; CESP:ZK328.3
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:ZK328.3
A:Introns: 63/1; 140/2; 419/1; 436/2; 488/2; 516/1; 545/2

Query Match 91.7%; Score 22; DB 2; Length 574;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 284 GTSTPS 289

RESULT 38

A96783
unknown protein F22H5.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A96783
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A96783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-593 <STO>
A:Cross-references: GB:AE005173; NID:g100923269; PIDN:AAG12682.1; GSPDB:GN00141
C:Genetics:
A:Gene: F22H5.2
A:Map position: 1

Query Match 91.7%; Score 22; DB 2; Length 593;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 22 GTSSPS 27

RESULT 39
T35746
Hypothetical protein SC7H2.15c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35746
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21588
A:Accession: T35746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-597 <SAU>
A:Cross-references: EMBL:AL109732; PIDN:CAB52057.1; GSPDB:GN00070; SCOEDB:SC7H2.15c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC7H2.15c

Query Match 91.7%; Score 22; DB 2; Length 597;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 299 GTATPS 304

RESULT 40
S20516
dnaK-type molecular chaperone hsp70, chloroplast - chromophytic alga (Pavlova lutheri
N:Alternate names: heat shock protein 70
C:Species: Chloroplast Pavlova lutheri
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S20516
R:Scaramuzzi, C.D.; Stokes, H.W.; Hiller, R.G.
Plant Mol. Biol. 18, 467-476, 1992
A:Title: Heat shock Hsp70 protein is chloroplast-encoded in the chromophytic alga Pav

A:Reference number: S20516; MUID:92163012

A:Accession: S20516

A:Molecule type: DNA

A:Residues: 1-629 <SCA>

A:Cross-references: EMBL:X59555; NID:g20904; PIDN:CAA42154.1; PID:g20905

C:Genetics:

A:Gene: hsp70

A:Genome: chloroplast

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein complex

C:Superfamily: heat shock protein 70

C:Keywords: ATP; chloroplast; molecular chaperone

Query Match 91.7%; Score 22; DB 2; Length 629;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

|| || ||

Db 33 GTTTPS 38

RESULT 41

A96781

unknown protein F9E10.5 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96781

R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: A96781

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-651 <STO>

A:Cross-references: GB:AE005173; NID:g6646755; PIDN:AAF21067.1; GSPDB:GN00141

C:Genetics:

A:Gene: F9E10.5

A:Map position: 1

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 651;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

|| || ||

Db 129 GTSPS 134

RESULT 42

B75622

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: B75622

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.J.;

M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: B75622

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-691 <WHI>

A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12628.1; PID:g6460924; TIGR:DR

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRB0037

A:Map position: megaplasmid

A:Genome: plasmid

A>Note: plasmid MP1

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 691;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

|| || ||

Db 563 GTTTPS 568

RESULT 43

T15152

hypothetical protein F35F10.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15152

R:Rohlfing, T.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid F35F10.

A:Reference number: Z18301

A:Accession: T15152

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-693 <ROH>

A:Cross-references: EMBL:AF002198; NID:g2076898; PID:g2076909; PIDN:AAB53997.1; GSPDB

A:Experimental source: strain Bristol N2; clone F35F10

C:Genetics:

A:Gene: CESP:F35F10.10

A:Map position: 5

A:Introns: 21/2; 65/1; 83/1; 169/3; 193/3; 235/3; 259/3; 289/1; 369/3; 412/3; 495/1;

Query Match

Best Local Similarity 91.7%; Score 22; DB 2; Length 693;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

|| || ||

Db 486 GTTTPS 491

RESULT 44

A29635

transcription factor Spl - human (fragment)

N:Alternate names: finger protein ZNF76

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 05-Nov-1999

C:Accession: A29635; G44256

R:Kadonaga, J.T.; Carner, K.R.; Maslars, F.R.; Tjian, R.

Cell 51, 1079-1090, 1987

A:Title: Isolation of cDNA encoding transcription factor Spl and functional analysis

A:Reference number: A29635; MUID:88080466

A:Accession: A29635

A:Molecule type: mRNA

A:Residues: 1-696 <KAD>

A:Cross-references: GB:J03133; NID:g339517; PIDN:AAA61154.1; PID:g339518

R:Ragoussis, J.; Senger, G.; Mockridge, I.; Sansau, P.; Ruddy, S.; Dudley, K.; Sheer

Genomics 14, 673-679, 1992

A:Title: A testis-expressed Zn finger gene (ZNF76) in human 6p21.3 centromeric to the

A:Reference number: A44256; MUID:93052398

A:Accession: G44256

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A;Residues: 569-598 <RAG>
A;Experimental source: T-cell line CEM
A;Note: sequence extracted from NCBI backbone (NCBIP:125980)
C;Genetics:
A;Gene: GDB:SP1
A;Cross-references: GDB:127453; OMIM:189906
A;Map position: 19q13.1-19q13.3
C;Keywords: DNA binding; transcription regulation; zinc finger

Query Match 91.7%; Score 22; DB 2; Length 696;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 647 GTATPS 652

RESULT 45

D96527
protein F77J15.24 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96527
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: D96527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-756 <STO>
A;Cross-references: GB:AE005173; NID:g7770335; PIDN:AAF69705.1; GSPDB:GN00141
C;Genetics:
A;Gene: F77J15.24
A;Map position: 1

Query Match 91.7%; Score 22; DB 2; Length 756;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 118 GTSSPS 123

RESULT 46

JS0747
regulatory protein Sp1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000
C;Accession: JS0747; S25287
R;Imataka, H.; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Hayami,
submitted to JIPID, September 1992
A;Reference number: JS0747
A;Accession: JS0747
A;Molecule type: mRNA
A;Residues: 1-788 <IMA>
A;Cross-references: DBJ:D12768; NID:g220911; PIDN:BAA02235.1; PID:d1002730; PID:g220912
R;Imataka, H.; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Hayami,
EMBO J. 11, 3663-3671, 1992
A;Title: Two regulatory proteins that bind to the basic transcription element (BTE), a G
A;Reference number: S25287; MUID:93010958
A;Accession: S25287

A;Molecule type: mRNA
A;Residues: 1-122, 'L', '124-311, 'A', 313-788 <IM2>
C;Keywords: DNA binding; transcription regulation

Query Match 91.7%; Score 22; DB 2; Length 788;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 739 GTATPS 744

RESULT 47

T28055
hypothetical protein ZK858.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28055
R;White, S.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z20462
A;Accession: T28055
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-848 <WIL>
A;Cross-references: EMBL:Z79759; PIDN:CAB02138.1; GSPDB:GN00019; CESP:ZK858.1
C;Experimental source: clone ZK858
C;Genetics:
A;Gene: CESP:ZK858.1
A;Map position: 1
A;Introns: 26/3; 82/3; 130/3; 195/3; 241/3; 613/1; 762/1

Query Match 91.7%; Score 22; DB 2; Length 848;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 630 GTAAPS 635

RESULT 48

T20429
hypothetical protein E03A3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20429
R;Gardner, A.
submitted to the EMBL Data Library, October 1994
A;Reference number: Z19274
A;Accession: T20429
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-875 <WIL>
A;Cross-references: EMBL:Z38112; PIDN:CAA86231.1; GSPDB:GN00021; CESP:E03A3.6
A;Experimental source: clone E03A3
C;Genetics:
A;Gene: CESP:E03A3.6
A;Map position: 3
A;Introns: 58/2; 161/3; 200/1; 257/3; 436/3; 629/3; 735/1; 762/3
C;Superfamily: Caenorhabditis elegans hypothetical protein E03A3.6

Query Match 91.7%; Score 22; DB 2; Length 875;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 827 GTSAPS 832

RESULT 49
A47521
capsid protein - giardiavirus GLV
C:Species: giardiavirus, GLV
C>Date: 21-Jan-1994 #sequence_revision 13-Feb-1998 #text_change 16-Jul-1999
C:Accession: A47521
R:Wang, A.L.; Yang, H.M.; Shen, K.A.; Wang, C.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 8595-8599, 1993
A:Title: Giardiavirus double-stranded RNA genome encodes a capsid polypeptide and a gag-
A:Reference number: A47521; MUID:93391401
A:Contents: host Giardia lamblia
A:Accession: A47521
A:Molecule type: genomic RNA
A:Residues: 1-886 <WAN>
A:Cross-references: GB:L13218; NID:q1352866; PIDN:AAB01578.1; PID:q1352867
A:Note: sequence modified after extraction from NCBI backbone (NCBIN:137593, NCBIP:13759
C:Superfamily: giardiavirus capsid protein
C:Keywords: capsid protein

Query Match 91.7%; Score 22; DB 1; Length 886;
Best Local Similarity 66.7%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
||
Db 796 GTAAPS 801

RESULT 50
T40290
hypothetical protein SPBC354.10 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40290
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: 221918
A:Accession: T40290
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-963 <WOO>
A:Cross-references: EMBL:AL022071; PIDN:CAAL7810.1; GSPDB:GN00067; SPDB:SPBC354.10
A:Experimental source: strain 972h-; cosmid c354
C:Genetics:
A:Gene: SPDB:SPBC354.10
A:Map position: 2

Query Match 91.7%; Score 22; DB 2; Length 963;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
||
Db 730 GTAPES 735

Search completed: September 3, 2002, 09:25:53
Job time: 45 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 09:25:58 ; Search time 10.34 seconds
(without alignments)
22.468 Million cell updates/sec

Title: BASK-853-CLAIM5

Perfect score: 24

Sequence: 1 gtxps 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	91.7	196	1	BCB_ARATH
2	22	91.7	255	1	YORE_PSECL
3	22	91.7	275	1	MYOD_BRARE
4	22	91.7	312	1	MTR7_MOUSE
5	22	91.7	379	1	VAT1_TORCA
6	22	91.7	389	1	CHS1_LXCES
7	22	91.7	389	1	CHS2_LXCES
8	22	91.7	389	1	CHS2_SOLTU
9	22	91.7	389	1	CHSA_SOLTU
10	22	91.7	389	1	CHSB_SOLTU
11	22	91.7	389	1	CHSJ_PETHY
12	22	91.7	389	1	CHSV_CATRO
13	22	91.7	389	1	CHSV_PRAVU
14	22	91.7	392	1	Y462_TREPA
15	22	91.7	395	1	CHS2_BETVE
16	22	91.7	397	1	CHS2_DAUCA
17	22	91.7	398	1	CHSV_CALCH
18	22	91.7	398	1	CHSV_PETCR
19	22	91.7	419	1	CHSD_PETHY
20	22	91.7	435	1	UGTB_CAEEL
21	22	91.7	629	1	DNAA_PAVLU
22	22	91.7	785	1	SPI_HUMAN
23	22	91.7	788	1	SPI_RAT
24	22	91.7	1050	1	ULK1_HUMAN
25	22	91.7	1262	1	GNR_MOUSE
26	22	91.7	1377	1	CID_DROME
27	22	91.7	2717	1	ZEP1_HUMAN
28	22	91.7	2769	1	THYG_BOVIN
29	21	87.5	45	1	LYS3_ECOLI
30	21	87.5	45	1	LYS3_SHISO
31	21	87.5	47	1	LYS2_ECOLI
32	21	87.5	47	1	LYS5_ECOLI
33	21	87.5	47	1	LYS6_ECOLI

ALIGNMENTS

RESULT 1

ID	BCB_ARATH	STANDARD;	PRT;	196 AA.
AC	Q07488;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Blue copper protein precursor.			
GN	BCB.			
OS	Arabidopsis thaliana (Mouse-ear cross).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV, COLUMBIA, AND CV. K85;			
RX	MEDLINE=94124044; PubMed=8294044;			
RA	van Gysel A., van Montagu M., Inze D.;			
RT	"A negatively light-regulated gene from Arabidopsis thaliana encodes			
RT	a protein showing high similarity to blue copper-binding proteins.";			
RL	Gene 136:79-85(1993).			
CC	!- FUNCTION: PROBABLY ACTS AS AN ELECTRON CARRIER.			
CC	!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	!- DEVELOPMENTAL STAGE: MAXIMUM LEVELS ARE FOUND IN 35 DAY OLD			
CC	PLANTLETS WHEN THE ROSETTE IS MATURE, CONSISTING OF 8-10 FULLY			
CC	EXPANDED LEAVES, AND AS THE FLORAL STEM STARTS TO FORM. THIS LEVEL			
CC	REMAINS CONSTANT DURING THE FURTHER LIFE SPAN OF THE PLANT.			
CC	!- INDUCTION: BY DARK ADAPTATION. THIS GIVES A 20-FOLD INCREASE IN			
CC	EXPRESSION.			
CC	!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; Z15058; CAA78771.1;			
DR	PIR; S25555; S25555.			
DR	HSSP; P29602; IJER.			
DR	InterPro; IPR000923; Copper_blue1.			
DR	InterPro; IPR003245; Cu_bind_1.			
DR	Pfam; PF02298; Cu_bind_like; 1.			
DR	ProDom; PD003122; Cu_bind_like; 1.			
DR	PROSITE; PS00196; COPPER_BLUE; 1.			
KW	Electron transport; Copper; Transmembrane; Signal; Metal-binding;			
KW	Glycoprotein.			
FT	SIGNAL	1	22	POTENTIAL.

Q03709 escherichia
P10099 escherichia
P15176 escherichia
P02987 escherichia
P09181 escherichia
P01306 gallus gall
P54499 bacillus su
Q00190 escherichia
P51304 porphyra pu
P25394 escherichia
P82805 arabidopsis
P75329 mycoplasma
Q10385 mycobacteri
P50355 rhizobium s
P55330 aspergillus
Q9RQV9 neisseria m
Q9K0V9 neisseria m

21 87.5 47 1 LYS7_ECOLI
21 87.5 47 1 LYS8_ECOLI
21 87.5 47 1 LYS9_ECOLI
21 87.5 49 1 LYS0_ECOLI
21 87.5 52 1 LYS4_ECOLI
21 87.5 80 1 PAHO_CHICK
21 87.5 94 1 YQGV_BACSU
21 87.5 118 1 TRH4_ECOLI
21 87.5 122 1 RK14_PORPU
21 87.5 170 1 FME7_ECOLI
21 87.5 187 1 OM24_ARATH
21 87.5 193 1 Y319_MYCPN
21 87.5 203 1 COX3_MYCTU
21 87.5 215 1 NOB8_RHISN
21 87.5 225 1 XYN2_ASPNG
21 87.5 242 1 PDX1_NEIMA
21 87.5 242 1 PDXJ_NEIMB

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FT CHAIN 23 196 BLUE COPPER PROTEIN.
 FT DOMAIN 23 118 PLASTOCYANIN-LIKE.
 FT TRANSMEM 119 143 POTENTIAL.
 FT TRANSMEM 173 189 POTENTIAL.
 FT DISULFID 79 113 BY SIMILARITY.
 FT METAL 66 66 COPPER (BY SIMILARITY).
 FT METAL 107 107 COPPER (BY SIMILARITY).
 FT METAL 112 112 COPPER (BY SIMILARITY).
 FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 196 AA; 20071 MW; 432D7270268F047A CRC64;

Query Match 91.7%; Score 22; DB 1; Length 196;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 158 GTTPS 163

RESULT 2

YORE_PSECL STANDARD; PRT; 255 AA.
 AC Q03003;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in P47K 3'region (ORFE) (Fragment).
 OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=333;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B23;
 RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
 RA Beppu T.;
 RT "Cloning and characterization of genes responsible for metabolism of
 RT nitrite compounds from Pseudomonas chlororaphis B23.";
 RL J. Bacteriol. 173:2465-2472(1991).
 CC -----

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EMBL; D90216; BAA14248.1; -
 DR PIR; E42725; E42725.
 DR InterPro; IPR001610; PAC.
 DR Pfam; PF00785; PAC; 1.
 DR SMART; SM00086; PAC; 1.
 KW Hypothetical protein.
 FT NON_TER 255 255
 SQ SEQUENCE 255 AA; 28905 MW; 073B230C8E38E0D2 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 255;
 Best Local Similarity 66.7%; Pred. No. 62;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 103 GTAAPS 108

RESULT 3

MYOD_BRARE STANDARD; PRT; 275 AA.
 ID MYOD_BRARE

Q90477;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Myoblast determination protein 1 homolog (Myogenic factor 1).
 GN MYOD.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96152221; PubMed=8565839;
 RA Weinberg E.S., Allende M.L., Kelly C.S., Abdelhamid A., Murakami T.,
 RA Andermann P., Doerre O.G., Grunwald D.J., Riggleman B.;
 RA "Developmental regulation of zebrafish MyoD in wild-type, no tail and
 RA spadetail embryos.";
 RT Development 122:271-280(1996).
 RL Development 122:271-280(1996).
 CC -!- FUNCTION: MYOGENESIS.
 CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION IS SPECIFIC TO THE MESODERM OF THE
 CC GASTRULA.
 CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.
 CC -----
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EMBL; Z36945; CAA85407.1; -
 DR HSP; P10085; IMDY.
 DR ZFIN; ZDB-GENE-980526-561; myod.
 DR InterPro; IPR002546; Basic.
 DR InterPro; IPR003015; HLH_Myc.
 DR InterPro; IPR001092; HLH_dim.
 DR Pfam; PF01586; Basic; 1.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00520; BASIC; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00038; HELIX LOOP HELIX; 1.
 DR Myogenesis; Differentiation; Developmental protein; Nuclear protein;
 KW Transcription regulation; DNA-binding.
 FT DNA_BIND 84 96 BASIC DOMAIN.
 FT DOMAIN 97 136 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 SQ SEQUENCE 275 AA; 30866 MW; 260091DDA756311C CRC64;

Query Match 91.7%; Score 22; DB 1; Length 275;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 253 GTTAPS 258

RESULT 4

MTR7_MOUSE STANDARD; PRT; 312 AA.
 ID MTR7_MOUSE

AC Q922C9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myotubularin related protein 7 (EC 3.1.3.48) (Fragment).
 DE MTR7.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98409499; PubMed=9736772;
RA Laporte J., Blondeau F., Bujo-Bello A., Tentler D., Kretz C., Dahl N.,
RA Mandel J.-L.;
RT "Characterization of the myotubularin dual specificity phosphatase
RT gene family from yeast to human.";
RL Hum. Mol. Genet. 7:1703-1712(1998).
CC -1- FUNCTION: NOT KNOWN, COULD BE A TYROSINE-PHOSPHATASE.
CC -1- SIMILARITY: BELONGS TO THE MYOTUBULARIN-LIKE FAMILY.
CC -----
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CC -----
DR EMBL; AF073882; AAC80004.1; -
DR MGD; MGI:1891693; Mtmr7.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR SMART; SM00012; PTPC_DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON_TER 1 1
FT ACT_SITE 48 48 BY SIMILARITY.
SQ SEQUENCE 312 AA; 36018 MW; 4BB40E0D15BD880C CRC64;

Query Match 91.7%; Score 22; DB 1; Length 312;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 294 GTASPS 299

RESULT 5
VATL TORCA
ID VATL_TORCA STANDARD; PRT; 379 AA.
AC P19333;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Synaptic vesicle membrane protein VAT-1.
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualia; Pristiogryae; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Electric lobe;
RX MEDLINE=90166593; PubMed=2483112;
RA Linial M., Miller K., Scheller R.H.;
RT "VAT-1: an abundant membrane protein from Torpedo cholinergic
RT synaptic vesicles.";
RL Neuron 2:1265-1273(1989).
CC -1- FUNCTION: MAY PLAY A CENTRAL ROLE IN THE FUNCTIONS MEDIATED BY
CC SPECIFIC CLASSES OF SYNAPTIC VESICLES.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: CHOLINERGIC SYNAPTIC VESICLES.
CC -1- MISCELLANEOUS: SYNTHESIZED IN THE NEURONAL CELL BODIES AND
CC TRANSPORTED TO THE TERMINALS. EACH VESICLE CONTAINS APPROXIMATELY
CC 28 MOLECULES OF VAT-1.
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE

CC FAMILY. QUINONE OXIDOREDUCTASE SUBFAMILY. STRONG, TO MAMMALIAN
CC VAT-1 HOMOLOGS.
DR PIR; JN0013; JN0013.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR002364; OOR_zeta_crystal.
DR Pfam; PF00107; adh_zinc; 1.
DR PROSITE; PS01162; OOR_ZETA_CRYSTAL; 1.
KW Oxidoreductase; Zinc; Synapse; Membrane; Phosphorylation.
FT MOD_RES 273 273 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 379 AA; 41593 MW; FA4ADAI7E657F09C CRC64;

Query Match 91.7%; Score 22; DB 1; Length 379;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 194 GTASPS 199

RESULT 6
CHSL LYCES
ID CHSL_LYCES STANDARD; PRT; 389 AA.
AC P23418;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chalcone synthase 1 (EC 2.3.1.74) (Naringenin-chalcone synthase 1).
GN CHSL.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon, Hypocotyl, and Leaf;
RX MEDLINE=91117196; PubMed=1980524;
RA O'Neill S.D., Tong Y., Spoerlein B., Forkmann G., Yoder J.I.;
RT "Molecular genetic analysis of chalcone synthase in Lycopersicon
RT esculentum and an anthocyanin-deficient mutant.";
RL Mol. Gen. Genet. 224:279-288(1990).
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONOIDS. A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55194; CAA38980.1; -
DR PIR; S12223; S12223.
DR InterPro; IPR001099; Chal_stil_synth.
DR Pfam; PF00195; Chal_stil_synth; 1.
DR Pfam; PF02797; Chal_stil_synth; 1.
DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
KW Flavonoid biosynthesis; Transferase; Acyltransferase;
KW Multigene family.
FT ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 389 AA; 42552 MW; 553DC69E5EA96A8B CRC64;

Query Match	91.7%;	Score 22;	DB 1;	Length 389;	
Best Local Similarity	66.7%;	Pred. No. 92;			
Matches	4;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
QY	1 gtxxps 6				
DB	23 GTSTPS 28				
RESULT	7				
CHS2_LYCES	STANDARD;	PRT;	389 AA.		
AC	P23419;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Chalcone synthase 2 (EC 2.3.1.74) (Naringenin-chalcone synthase 2).				
GN	CHS2				
OS	Lycopersicon esculentum (Tomato).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.				
OX	NCBI_TaxID=4081;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Cotyledon, Hypocotyl, and Leaf;				
RC	MEDLINE=91117196; PubMed=1980524;				
RA	O'Neill S.D., Tong Y., Spoerlein B., Forkmann G., Yoder J.I.;				
RT	"Molecular genetic analysis of chalcone synthase in Lycopersicon				
RT	esculentum and an anthocyanin-deficient mutant.";				
RL	Mol. Gen. Genet. 224:279-288(1990).				
CC	-!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-				
CC	TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)				
CC	WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO				
CC	NARINGENIN.				
CC	-!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +				
CC	naringenin-chalcone + 3 CO(2).				
CC	-!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF				
CC	FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY				
CC	OF WHICH ARE BRIGHTLY COLORED.				
CC	-!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.				
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CC	or send an email to license@isb-sib.ch).				
CC	-!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +				
CC	naringenin-chalcone + 3 CO(2).				
CC	-!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF				
CC	FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY				
CC	OF WHICH ARE BRIGHTLY COLORED.				
CC	-!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.				
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CC	or send an email to license@isb-sib.ch).				
CC	EMBL; X55195; CAA38981.1; -				
DR	PIR; S12224; S12224.				
DR	InterPro; IPR001099; Chal_stil_synt.				
DR	Pfam; PF00195; Chal_stil_synt; 1.				
DR	Pfam; PF02797; Chal_stil_syntC; 1.				
DR	PROSITE; PS00441; CHALCONE_SYNTH; 1.				
DR	Flavonoid biosynthesis; Transferase; Acyltransferase;				
KW	Multigene family.				
KW	ACT_SITE 164				
FT	BY SIMILARITY.				
FT	SEQUENCE 389 AA; 42730 MW; F92E46BB3B5FC32F CRC64;				
SQ					
Query Match	91.7%;	Score 22;	DB 1;	Length 389;	
Best Local Similarity	66.7%;	Pred. No. 92;			
Matches	4;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
QY	1 gtxxps 6				
DB	23 GTSTPS 28				
RESULT	8				
CHS2_LYCES	STANDARD;	PRT;	389 AA.		
AC	P23419;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Chalcone synthase 2 (EC 2.3.1.74) (Naringenin-chalcone synthase 2).				
GN	CHS2				
OS	Lycopersicon esculentum (Tomato).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC					

```

RP SEQUENCE FROM N.A.
RC STRAIN-CV. RED PONTIAC;
RA Jeon J.-H., Kim H.-S., Choi K.-H., Joung Y.-H., Joung H., Byun S.-M.;
RT "Characterization of two members of the chalcone synthase gene family
RT from Solanum tuberosum L.";
RL (In) Plant Gene Register PGR96-027.
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONONDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC
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CC -----
DR EMBL; U47739; AAB67734.1; -.
DR Mendel; 10624; SOLTU;1193;1.
DR InterPro; IPR001099; Chal_stil_synt.
DR Pfam; PF001195; Chal_stil_synt; 1.
DR Pfam; PF02797; Chal_stil_synt; 1.
DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
KW Flavonoid biosynthesis; Transferase; Acyltransferase;
KW Multigene family.
FT ACT_SITE 164 BY SIMILARITY.
SQ SEQUENCE 389 AA; 42562 MW; B181D9C6B9170A34 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 389;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 23 GTSTPS 28

RESULT 10
CHSB_SOLTU STANDARD; PRT; 389 AA.
AC Q43163;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chalcone synthase 1B (EC 2.3.1.74) (Naringenin-chalcone synthase 1B).
GN CHS1B.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. RED PONTIAC;
RA Jeon J.-H., Kim H.-S., Choi K.-H., Joung Y.-H., Joung H., Byun S.-M.;
RT "Characterization of two members of the chalcone synthase gene family
RT from Solanum tuberosum L.";
RL (In) Plant Gene Register PGR96-027.
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).

```

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CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONONDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC
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CC -----
DR EMBL; U47740; AAB67735.1; -.
DR Mendel; 10625; SOLTU;1193;2.
DR InterPro; IPR001099; Chal_stil_synt.
DR Pfam; PF001195; Chal_stil_synt; 1.
DR Pfam; PF02797; Chal_stil_synt; 1.
DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
KW Flavonoid biosynthesis; Transferase; Acyltransferase;
KW Multigene family.
FT ACT_SITE 164 BY SIMILARITY.
SQ SEQUENCE 389 AA; 42548 MW; E7334A1A34D8D1CC CRC64;

Query Match 91.7%; Score 22; DB 1; Length 389;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 23 GTSTPS 28

RESULT 11
CHSJ_PETHY STANDARD; PRT; 389 AA.
AC P29228;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chalcone synthase J (EC 2.3.1.74) (Naringenin-chalcone synthase J).
GN CHSJ.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. VIOLET 30; TISSUE=Leaf;
RX MEDLINE=90034197; PubMed=2806915;
RA Koes R.E., Spelt C.E., van den Elzen P.J.M., Mol J.N.M.;
RT "Cloning and molecular characterization of the chalcone synthase
RT multigene family of Petunia hybrida.";
RL Gene 81:245-257(1989).
RN [2]
RP SEQUENCE OF 71-389 FROM N.A.
RC STRAIN-CV. WHITE 137; TISSUE=Anther;
RA van Tunen A.J.;
RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONONDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC
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 CC -----

DR EMBL; X14597; CAA32737.1; -;
 DR EMBL; X14599; CAA32739.1; -;
 DR PIR; JS0309; SYPJGJ.
 DR InterPro; IPR001099; Chal_stil_synt.
 DR Pfam; PF00195; Chal_stil_synt; 1.
 DR Pfam; PF02797; Chal_stil_syntC; 1.
 DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
 DR Flavonoid biosynthesis; Transferase; Acyltransferase;
 KW Multigene family. 164 BY SIMILARITY.
 FT ACT_SITE 75 E -> V (IN REF. 2).
 FT CONFLICT 75
 SQ SEQUENCE 389 AA; 42558 MW; F2B3CDD82E6FDE7D CRC64;

Query Match 91.7%; Score 22; DB 1; Length 389;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 DB 23 GTATPS 28

RESULT 12
 CHSY_CATRO STANDARD; PRT; 389 AA.
 ID CHSY_CATRO STANDARD; PRT; 389 AA.
 AC Q9ZRS4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase).
 GN CHS.
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
 CC Vinceae; Catharanthus.
 CC NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kaltenbach M., Schroeder G., Schmelzer E., Lutz V., Schroeder J.;
 RT "Flavonoid hydroxylase from Catharanthus roseus: cDNA, heterologous
 RT expression, enzyme properties, and cell-type specific expression in
 RT plants.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
 CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
 CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
 CC NARINGENIN.
 CC -!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
 CC naringenin-chalcone + 3 CO(2).
 CC -!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
 CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
 CC OF WHICH ARE BRIGHTLY COLORED.
 CC -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ131813; CAA10511.1; -;
 DR Mendel; 36879; Catro; I193; 36879.

DR InterPro; IPR001099; Chal_stil_synt.
 DR Pfam; PF00195; Chal_stil_synt; 1.
 DR Pfam; PF02797; Chal_stil_syntC; 1.
 DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
 KW Flavonoid biosynthesis; Transferase; Acyltransferase.
 FT ACT_SITE 164 BY SIMILARITY.
 SQ SEQUENCE 389 AA; 42492 MW; B350742DB4A19186 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 389;
 Best Local Similarity 66.7%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 DB 23 GTSTPS 28

RESULT 13
 CHSY_PHAVU STANDARD; PRT; 389 AA.
 ID CHSY_PHAVU STANDARD; PRT; 389 AA.
 AC P49440;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Chalcone synthase 17 (EC 2.3.1.74) (Naringenin-chalcone synthase 17).
 GN CHS17.
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 CC NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. CANADIAN WONDER;
 RX MEDLINE=88142539; PubMed=3481420;
 RA Ryder T.B., Hedrick S.A., Bell J.N., Liang X., Clouse S.D.,
 RA Lamb C.J.;
 RT "Organization and differential activation of a gene family encoding
 RT the plant defense enzyme chalcone synthase in Phaseolus vulgaris.";
 RL Mol. Gen. Genet. 210:219-233(1987).
 CC -!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
 CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
 CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
 CC NARINGENIN.
 CC -!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
 CC naringenin-chalcone + 3 CO(2).
 CC -!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
 CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
 CC OF WHICH ARE BRIGHTLY COLORED.
 CC -!- INDUCTION: BY IRRADIATION, ELICITOR, INFECTION OR WOUNDING.
 CC -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
 CC -----
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 CC -----
 DR EMBL; X06411; CAA29700.1; -;
 DR InterPro; IPR001099; Chal_stil_synt.
 DR Pfam; PF00195; Chal_stil_synt; 1.
 DR Pfam; PF02797; Chal_stil_syntC; 1.
 DR PROSITE; PS00441; CHALCONE_SYNTH; 1.
 KW Flavonoid biosynthesis; Transferase; Acyltransferase;
 KW Multigene family. 164 BY SIMILARITY.
 FT ACT_SITE 164
 SQ SEQUENCE 389 AA; 42654 MW; 25F13C3C4D654F47 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 389;

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Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 23 GTATPS 28

RESULT 14
Y462_TREPA
ID Y462_TREPA STANDARD; PRT; 392 AA.
AC 083475; 083476;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein TP0462/TP0463 precursor.
GN TP0462/TP0463
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Ariach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RL Spirochete.";
RL Science 281:375-388(1998).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE TP013X FAMILY OF LIPOPROTEINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. REF.1 SEQUENCE DIFFERS
CC FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 279.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001223; AAC65455.1; ALT_FRAME.
DR EMBL; AE001223; AAC65456.1; ALT_FRAME.
DR TIGR; TP0462; -.
DR TIGR; TP0463; -.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Lipoprotein; Membrane; Signal;
KW complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 392 HYPOTHETICAL LIPOPROTEIN TP0462/TP0463.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 148 163 GLY/SER-RICH.
SQ SEQUENCE 392 AA; 40261 MW; F2689260172607AE CRC64;

Query Match 91.7%; Score 22; DB 1; Length 392;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 116 GTTPS 121

RESULT 15
CHSY_BETVE
ID Y462_TREPA STANDARD; PRT; 392 AA.
AC 083475; 083476;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein TP0462/TP0463 precursor.
GN TP0462/TP0463
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Ariach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RL Spirochete.";
RL Science 281:375-388(1998).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE TP013X FAMILY OF LIPOPROTEINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. REF.1 SEQUENCE DIFFERS
CC FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 279.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001223; AAC65455.1; ALT_FRAME.
DR EMBL; AE001223; AAC65456.1; ALT_FRAME.
DR TIGR; TP0462; -.
DR TIGR; TP0463; -.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Lipoprotein; Membrane; Signal;
KW complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 392 HYPOTHETICAL LIPOPROTEIN TP0462/TP0463.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 148 163 GLY/SER-RICH.
SQ SEQUENCE 392 AA; 40261 MW; F2689260172607AE CRC64;

Query Match 91.7%; Score 22; DB 1; Length 395;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 23 GTATPS 28

RESULT 16
CHS2_DAUCA
ID CHS2_DAUCA STANDARD; PRT; 397 AA.
AC 092540;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chalcone synthase 2 (EC 2.3.1.74) (Naringenin-chalcone synthase 2).

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GN CHS2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirner A.A., Seitz H.U.;
RT "Cloning of two different chalcone synthase isoforms from Daucus
RT carota L. and their differential expression in organs from european
RT wild carrot and in UV-A irradiated cell cultures.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
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CC -----
CC EMBL; AJ206780; CAA07245.1; -.
CC InterPro: IPR001099; Chal_stil_synth.
CC Pfam: PF00195; Chal_stil_synth; 1.
CC ProSITE; PS00441; CHALCONE_SYNTH; 1.
CC Flavanoid biosynthesis; Transferase; Acyltransferase;
CC ACT_SITE 168 BY SIMILARITY.
CC MULTIGENE FAMILY.
CC FT ACT_SITE 168
CC SEQUENCE 397 AA; 43559 MW; 9386F44B9132EDEE CRC64;

Query Match 91.7%; Score 22; DB 1; Length 397;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 27 GTATPS 32

RESULT 17
CHSY_CALCH STANDARD; PRT; 398 AA.
AC P48385;
DT 01-FEB-1996 (Rel. 33; Created)
DT 15-DEC-1998 (Rel. 37; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase).
GN CHS.
OS Callistephus chinensis (China aster).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Astereae; Callistephus.
OX NCBI_TaxID=13379;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L 01; TISSUE=Petal;
RA Henkel J., Wassenecker M., Sommer H., Forkmann G.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

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CC -!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
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CC -----
CC EMBL; Z67988; CAA91930.1; -.
CC InterPro: IPR001099; Chal_stil_synth.
CC Pfam: PF00195; Chal_stil_synth; 1.
CC ProSITE; PS00441; CHALCONE_SYNTH; 1.
CC Flavanoid biosynthesis; Transferase; Acyltransferase.
CC ACT_SITE 167 BY SIMILARITY.
CC SEQUENCE 398 AA; 43541 MW; 8B7D4E11B4FAFFC3 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 398;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 26 GTATPS 31

RESULT 18
CHSY_PETCR STANDARD; PRT; 398 AA.
AC P16107;
DT 01-APR-1990 (Rel. 14; Created)
DT 01-APR-1990 (Rel. 14; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase).
GN CHS.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.
RA Reimold U., Kroeger M., Kreuzaler F., Hahlbrock K.;
RT "Coding and 3' non-coding nucleotide sequence of chalcone synthase
RT mRNA and assignment of amino acid sequence of the enzyme.";
RL EMBO J. 2:1801-1805(1983).
CC -!- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -!- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2).
CC -!- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
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EMBL: V01538; CAA24779.1; -
PIR: S42523; S42523.
InterPro: IPR001099; Chal_stil_synth.
Pfam: PF00195; Chal_stil_synth; 1.
Pfam: PF02797; Chal_stil_synth; 1.
PROSITE: PS00441; CHALCONE_SYNTH; 1.
Flavonoid biosynthesis; Transferase; Acyltransferase.
FT ACT_SITE 169 169 BY SIMILARITY.
SQ SEQUENCE 398 AA; 43735 MW; E8B19149AD3DABIE CRC64;

Query Match 91.7%; Score 22; DB 1; Length 398;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 gtxxps 6
Db 28 GTATPS 33

RESULT 19
CHSD_PETHY STANDARD; PRT; 419 AA.
AC P22925;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chalcone synthase D (EC 2.3.1.74) (Naringenin-chalcone synthase D).
GN CHSD.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, VIOLET 30; TISSUE=Leaf;
RX MEDLINE=90034197; PubMed=2806915;
RA Koes R.E., Spelt C.E., van den Elzen P.J.M., Mol J.N.M.;
RT "Cloning and molecular characterization of the chalcone synthase
multigene family of Petunia hybrida.";
RL Gene 81:245-257(1989).
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4',2',4',6'-
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
naringenin-chalcone + 3 CO(2).
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
OF WHICH ARE BRIGHTLY COLORED.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
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EMBL: X14593; CAA32733.1; -
PIR: JS0312; SYPJCD.
InterPro: IPR001099; Chal_stil_synth.
Pfam: PF00195; Chal_stil_synth; 1.
Pfam: PF02797; Chal_stil_synth; 1.
PROSITE: PS00441; CHALCONE_SYNTH; 1.
Flavonoid biosynthesis; Transferase; Acyltransferase;
KW Multigene family.

FT ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 419 AA; 45979 MW; 55827338DC812ACD CRC64;

Query Match 91.7%; Score 22; DB 1; Length 419;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 gtxxps 6
Db 23 GTATPS 28

RESULT 20
UGTB_CAEEL STANDARD; PRT; 435 AA.
ID UGTB_CAEEL
AC Q22180;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative UDP-glucuronosyltransferase UGT11 (EC 2.4.1.17) (UDPGT).
GN UGT11 OR T04H1.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Harris B.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
beta-D-glucuronoside.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

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EMBL: Z78200; CAB01584.1; -
WormPep: T04H1.7; CE13179.
InterPro: IPR002213; UDPGT.
Pfam: PF00201; UDPGT; 1.
PROSITE: PS00375; UDPGT; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Multigene family.
SQ SEQUENCE 435 AA; 50020 MW; AF04A0DE7208CBF3 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 435;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 gtxxps 6
Db 300 GTTTPS 305

RESULT 21
DNAK_PAVLU STANDARD; PRT; 629 AA.
ID DNAK_PAVLU
AC P30722;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
protein) (HSP70).
GN DNAK OR HSP70.
OS Pavlova lutherii (Monochrysis lutheri).


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RESULT 23
SPL_RAT
ID SPL_RAT STANDARD; PRT; 788 AA.
AC Q01714;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor Spl.
GN SPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93010958; PubMed=1356762;
RA Imataka H., Sogawa K., Yasumoto K., Kikuchi Y., Sasano K.,
RA Kobayashi A., Hayami M., Fujii-Kuriyama Y.;
RT "Two regulatory proteins that bind to the basic transcription element
RT (BTE), a GC box sequence in the promoter region of the rat P-4501A1
RT gene.";
RL EMBL J. 11:3663-3671(1992).
CC -!- FUNCTION: BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY
CC ACTIVATES MRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL
CC RECOGNITION SITES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- PTM: O-GLYCOSYLATED; CONTAINS N-ACETYLGLUCOSAMINE SIDE CHAINS
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SPL FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -----
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CC -----
DR EMBL; D12768; BAA02235.1; -.
DR PIR; J50747; JS0747.
DR HSP; P08047; ISP1.
DR TRANSFAC; T00754; -.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF000096; zf-C2H2; 3.
DR PRINTS; PR00048; ZNCFINGER.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW DNA-binding; Nuclear protein; Repeat; Glycoprotein.
FT DOMAIN 629 711 ZINC FINGERS.
FT ZN_FING 629 653 C2H2-TYPE.
FT ZN_FING 659 683 C2H2-TYPE.
FT ZN_FING 689 711 C2H2-TYPE.
SQ SEQUENCE 788 AA; 81015 MW; AA2B0CAB81AAB80C CRC64;

Query Match 91.7%; Score 22; DB 1; Length 788;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 739 GTATPS 744

RESULT 24
ULK1_HUMAN
ID ULK1_HUMAN STANDARD; PRT; 1050 AA.
AC O75385;

Query Match 91.7%; Score 22; DB 1; Length 1050;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 745 GTSSPS 750

RESULT 25
GNRP_MOUSE
ID GNRP_MOUSE STANDARD; PRT; 1262 AA.
AC P27671;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Guanine nucleotide releasing protein (GNRP) (Ras-specific nucleotide
DE exchange factor CDC25) (CDC25Mm).
DE RASGRF1 OR CDC25 OR GRF1.
GN RASGRF1 OR CDC25 OR GRF1.

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase ULK1 (EC 2.7.1.-) (Unc-51-like kinase
DE 1).
GN ULK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98360094; PubMed=9693035;
RA Kuroyanagi H., Yan J., Seki N., Yamanouchi Y., Suzuki Y.-I.,
RA Takano T., Muramatsu M.-A., Shirasawa T.;
RT "Human ULK1, a novel serine/threonine kinase related to UNC-51 kinase
RT of Caenorhabditis elegans: cDNA cloning, expression, and chromosomal
RT assignment.";
RL Genomics 51:76-85(1998).
CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. DETECTED IN THE
CC FOLLOWING ADULT TISSUES: SKELETAL MUSCLE, HEART, PANCREAS, BRAIN,
CC PLACENTA, LIVER, KIDNEY, AND LUNG.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC APG1/UNC-51/ULK1 SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF045458; AAC32326.1; -.
DR HSP; P00523; 2PTK.
DR MIM; 603168; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 278 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 46 46 ATP (BY SIMILARITY).
FT ACT_SITE 138 138 BY SIMILARITY.
FT DOMAIN 297 310 POLY-SER.
SQ SEQUENCE 1050 AA; 112601 MW; 4ED9B94028E3C138 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 1050;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 745 GTSSPS 750
```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93010996; PubMed=1396590;
RA Cen H., Lowy D.D.;
RT "Isolation of multiple mouse cDNAs with coding homology to
RT Saccharomyces cerevisiae CDC25: identification of a region related to
RT Bcr, Vav, Dbl and CDC24";
RL EMBO J. 11:4007-4015(1992).
RN [2]
RP SEQUENCE OF 791-1262 FROM N.A.
RX MEDLINE=92357779; PubMed=1379731;
RA Wei W., Mosteller R.D., Sanyal P., Gonzales E., McKinney D.,
RA Dasgupta C., Li P., Liu B.X., Broek D.;
RT "Identification of a mammalian gene structurally and functionally
RT related to the CDC25 gene of Saccharomyces cerevisiae";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7100-7104(1992).
CC -!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: CONTAINS 2 PH DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 DEL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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CC
DR EMBL; L20899; AAA02741.1; -
DR EMBL; X59868; CAA42525.1; -
DR PIR; S20730; S20730.
DR PIR; S22693; S22693.
DR MGI; 99694; Rasgrf1.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR001895; RasGEF_CDC25.
DR InterPro; IPR000219; RHOGEF.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00169; PH; 2.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEFN; 1.
DR Pfam; PF00621; RHOGEF; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00233; PH; 2.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 2.
DR SMART; SM00325; RHOGEF; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00720; GDS_CDC25; 1.
DR PROSITE; PS50096; IQ; 1.
DR PROSITE; PS50003; PH_DOMAIN; 2.
KW Guanine-nucleotide releasing factor; Repeat.
FT DOMAIN 22 130

FT DOMAIN 208 233 IQ.
FT DOMAIN 244 430 DH.
FT DOMAIN 460 588 PH 2.
FT DOMAIN 1025 1259 RASGEF.
FT CONFLICT 1033 1033 E -> D. (IN REF. 3).
SQ SEQUENCE 1262 AA; 144101 MW; 38BFE68F/C228DC8 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 1262;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 734 GTSSPS 739

RESULT 26
CID_DROME
ID CID_DROME STANDARD; PRT; 1377 AA.
AC P19538;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Cubitus interruptus dominant protein.
GN CI-D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=90346286; PubMed=2166702;
RA Orenic T.V., Slusarski D.C., Kroll K.L., Holmgren R.A.;
RT "Cloning and characterization of the segment polarity gene cubitus
RT interruptus dominant of Drosophila";
RL Genes Dev. 4:1053-1067(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92146935; PubMed=1686006;
RA Berry A.J., Ajiloka J.W., Kreitman M.;
RT "Lack of polymorphism on the Drosophila fourth chromosome resulting
RT from selection";
RL Genetics 129:1111-1117(1991).
CC -!- FUNCTION: INVOLVED IN SEGMENT POLARITY. IS REQUIRED FOR THE NORMAL
CC DEVELOPMENT OF THE POSTERIOR HALF OF EACH EMBRYONIC SEGMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED UNIFORMLY THROUGHOUT THE BLASTODERM
CC STAGE AND GASTRULATION AND DOES NOT RESOLVE INTO SEGMENTALLY
CC REPEATING STRIPES UNTIL THE END OF THE SHORT PHASE OF GERM-BAND
CC EXTENSION.
CC -!- SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS
CC PROTEINS.
CC
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CC
DR EMBL; X54360; CAA38244.1; -
DR PIR; A35817; A35817.
DR PIR; S12769; S12769.
DR HSSP; P08151; 2GLI.
DR FlyBase; FBgn0004859; ci.
DR InterPro; IPR000822; znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR PRINTS; PR00048; ZINC-FINGER.
DR

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DR SMART; SM00355; Znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW Developmental protein; Segmentation polarity protein; Zinc-finger;
KW Metal-binding; DNA-binding; Repeat; Nuclear protein.
FT DOMAIN 451 603 ZINC_FINGERS.
FT ZN_FING 451 476 C2H2-TYPE.
FT ZN_FING 484 511 C2H2-TYPE.
FT ZN_FING 517 541 C2H2-TYPE.
FT ZN_FING 547 572 C2H2-TYPE.
FT ZN_FING 578 603 C2H2-TYPE.
SQ SEQUENCE 1377 AA; 150881 MW; 85189314D5E7B3B7 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 1377;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 655 GTSPS 660

RESULT 27
ZEP1_HUMAN STANDARD; PRT; 2717 AA.
AC P15822;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
DE binding protein 1) (HIV-1) (Major histocompatibility complex binding
DE protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
DE (PRDII-BF1)
DE HIVEP1 OR ZNF40.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169514; PubMed=2106471;
RA Fan C.M., Maniatis T.;
RT "A DNA-binding protein containing two widely separated zinc finger
RT motifs that recognize the same DNA sequence.";
RL Genes Dev. 4:29-42(1990).
RN [2]
RP STRUCTURE BY NMR OF 2113-2142.
RX MEDLINE=91064333; PubMed=2248949;
RA Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
RA Gronenborn A.M.;
RT "High-resolution three-dimensional structure of a single zinc finger
RT from a human enhancer binding protein in solution.";
RL Biochemistry 29:9324-9334(1990).
RN [3]
RP STRUCTURE BY NMR OF 2087-2142.
RX MEDLINE=92232684; PubMed=1567844;
RA Omichinski J.G., Clore G.M., Roblen M., Sakaguchi K., Appella E.,
RA Gronenborn A.M.;
RT "High-resolution solution structure of the double Cys2His2 zinc
RT finger from the human enhancer binding protein MBP-1.";
RL Biochemistry 31:3907-3917(1992).
CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC 5'-GGGACTTTC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC IN T-CELL ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC -1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
CC SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
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CC SMART; SM00355; Znf_C2H2; 5.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
CC PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
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CC -----
CC EMBL; X51435; CAA35798.1; -.
CC PIR; A34203; A34203.
CC PDB; 3ZNF; 15-JAN-92.
CC PDB; 4ZNF; 15-JAN-92.
CC PDB; 1BBO; 31-OCT-93.
CC TRANSFAC; T00497; -.
CC MIN; 194540; -.
CC InterPro; IPR000822; Znf-C2H2.
CC PRINTS; PR00096; zf-C2H2; 5.
CC PRINTS; PR00048; ZINCFINGER.
CC SMART; SM00355; Znf_C2H2; 4.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
CC PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
CC Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
CC Nuclear protein; Repeat; 3D-structure.
CC DOMAIN 406 456 ZINC_FINGERS.
CC ZN_FING 406 428 C2H2-TYPE.
CC ZN_FING 434 456 C2H2-TYPE.
CC DOMAIN 803 806 POLY-SER.
CC ZN_FING 958 981 C2HC-TYPE (POTENTIAL).
CC DOMAIN 2087 2139 ZINC_FINGERS.
CC ZN_FING 2087 2109 C2H2-TYPE.
CC ZN_FING 2115 2139 C2H2-TYPE.
CC STRAND 2088 2088
CC TURN 2090 2092
CC STRAND 2095 2095
CC STRAND 2099 2108
CC TURN 2109 2109
CC STRAND 2115 2116
CC STRAND 2123 2124
CC HELIX 2127 2135
SQ SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;

Query Match 91.7%; Score 22; DB 1; Length 2717;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 185 GTSPS 190

RESULT 28
THYG_BOVIN STANDARD; PRT; 2769 AA.
ID THYG_BOVIN STANDARD; PRT; 2769 AA.
AC P01267; Q18976; Q95478; Q28196;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyroglobulin precursor.
GN TG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85296288; PubMed=3855243;
RA Mercken L., Simons M.-J., Swillens S., Massaer M., Vassart G.;
RT "Primary structure of bovine thyroglobulin deduced from the sequence
```

RT of its 8,431-base complementary DNA.";

RL Nature 316:647-651(1985).

RN [2]

RP SEQUENCE OF 1-930 FROM N.A.

RX MEDLINE-85127025; PubMed-3855750;

RA Mercken L., Simons M.-J., de Martynhoff G., Swillens S., Vassart G.;

RT "Presence of hormonogenic and repetitive domains in the first 930

RT amino acids of bovine thyroglobulin as deduced from the cDNA

RT sequence.";

RL Eur. J. Biochem. 147:59-64(1985).

RN [3]

RP SEQUENCE OF 1-22 FROM N.A.

RX MEDLINE-87190432; PubMed-3032624;

RA de Martynhoff G., Pohl V., Mercken L., van Ommen G.-J., Vassart G.;

RT "Structural organization of the bovine thyroglobulin gene and of its

RT 5'-flanking region.";

RL Eur. J. Biochem. 164:591-599(1987).

RN [4]

RP SEQUENCE OF 1002-1209 FROM N.A.

RX MEDLINE-88062712; PubMed-3681978;

RA Parma J., Christophe D., Pohl V., Vassart G.;

RT "Structural organization of the 5' region of the thyroglobulin gene.

RT Evidence for intron loss and 'exonization' during evolution.";

RL J. Mol. Biol. 196:769-779(1987).

CC -!- FUNCTION: PRECURSOR OF THE IODINATED THYROID HORMONES THYROXINE

CC (T4) AND TRIIODOTHYRONINE (T3).

CC -!- SUBUNIT: HOMODIMER.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: THYROID GLAND SPECIFIC.

CC -!- PTM: SULFATED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

CC -!- SIMILARITY: CONTAINS 11 THYROGLOBULIN TYPE-I DOMAINS.

CC -----

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CC -----

DR EMBL; X02815; CAA26584.1; -

DR EMBL; X02155; CAA26090.1; -

DR EMBL; X05380; CAA28971.1; ALT_SEQ.

DR EMBL; X06071; CAA29457.1; -

DR EMBL; X06072; CAA29457.1; JOINED.

DR EMBL; X06073; CAA29457.1; JOINED.

DR EMBL; X06074; CAA29457.1; JOINED.

DR EMBL; X06075; CAA29457.1; JOINED.

DR PIR; A01533; UIBO.

DR HSSP; P21836; IMAA.

DR InterPro; IPR002018; Carboxylesterase_B.

DR InterPro; IPR000716; Thyroglobulin_1.

DR Pfam; PF00135; Coesterase; 2.

DR Pfam; PF00086; thyroglobulin_1; 8.

DR SMART; SM00211; TV; 10.

DR SMART; X06071; TV; 10.

DR PROSITE; PS00484; THYROGLOBULIN_1; 9.

DR PROSITE; PS00941; CARBOXYLESTERASE_B; 2; 1.

KW Glycoprotein; Repeat; Thyroid hormone; Iodination; Sulfation; Signal.

FT SIGNAL 1 19

FT CHAIN 20 2769

FT DOMAIN 31 92

FT DOMAIN 93 160

FT DOMAIN 161 297

FT DOMAIN 298 358

FT DOMAIN 604 657

FT DOMAIN 661 725

FT DOMAIN 726 921

FT DOMAIN 922 1073

FT DOMAIN 1074 1145

FT DOMAIN 1146 1210

FT DOMAIN 1458 1471

FT REPEAT 1472 1488

FT TYPE II.

FT REPEAT 1489 1505

FT DOMAIN 1513 1567

FT REPEAT 1605 1725

FT REPEAT 1726 1893

FT REPEAT 1894 1996

FT REPEAT 1997 2130

FT REPEAT 2131 2188

FT MOD_RES 24 24

FT MOD_RES 24 24

FT MOD_RES 2574 2574

FT MOD_RES 2588 2588

FT MOD_RES 2767 2767

FT CARBOHYD 110 110

FT CARBOHYD 198 198

FT CARBOHYD 483 483

FT CARBOHYD 495 495

FT CARBOHYD 747 747

FT CARBOHYD 853 853

FT CARBOHYD 947 947

FT CARBOHYD 1140 1140

FT CARBOHYD 1365 1365

FT CARBOHYD 1776 1776

FT CARBOHYD 1870 1870

FT CARBOHYD 2014 2014

FT CARBOHYD 2123 2123

FT CARBOHYD 2251 2251

FT CARBOHYD 2296 2296

FT CONFLICT 1206 1206

SQ SEQUENCE 2769 AA; 303218 MW; 1C7F227E9101DE2A CRC64;

Query Match 91.7%; Score 22; DB 1; Length 2769;

Best Local Similarity 66.7%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

DB 2196 GrSSPS 2201

RESULT 29

LYS3_ECOLI STANDARD; PRT; 45 AA.

ID LYS3_ECOLI

AC P05821;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lysis protein for colicin E1 precursor.

GN LYS.

OS Escherichia coli.

OG Plasmid ColE1.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_Taxid=562;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-86094231; PubMed-3936034;

RA Waleh N.S.; Johnson P.H.;

RT "Structural and functional organization of the colicin E1 operon.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-EC31, AND EC71;

RX MEDLINE-95062249; PubMed-7972047;

RA Riley M.A., Tan Y., Wang J.;

RT "Nucleotide polymorphism in colicin E1 and Ia plasmids from natural

RT isolates of Escherichia coli.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:11276-11280(1994).

CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE

CC AND PARTIAL CELL LYSIS.

CC -----

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DR EMBL; M12543; AAA23067.1; -;
DR EMBL; U15629; AAA59411.1; -;
DR EMBL; U15633; AAA59419.1; -;
DR PIR; B24685; ZHECP1.
DR Pfam; PF02402; Lysis_col.
DR InterPro; IPR003059; Lysis_col.
DR PRISM; PR01297; LYSISCOLICIN.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW PLASMID; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 45
FT LIPID 18 18
SQ SEQUENCE 45 AA; 4829 MW; A34D3B4FBC12A13E CRC64;

Query Match 87.5%; Score 21; DB 1; Length 45;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 29 GTIAPS 34

RESULT 30
LYS3_SHISO STANDARD; PRT; 45 AA.
AC P21185;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E1* precursor.
GN KIL.

OS Shigella sonnei.
OG plasmid pKY-1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=624;
[1]

SEQUENCE FROM N.A.
RA Higashi M., Hata M., Hase T., Yamaguchi K., Masamune Y.;
RT "The nucleotide sequence of cea and the region of origin of plasmid
pKY-1.";
RL J. Gen. Appl. Microbiol. 32:433-442(1986).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
AND PARTIAL CELL LYSIS.

CC -!- SIMILARITY: 96% IDENTITY TO E. COLI LYSIS PROTEIN PRECURSOR.

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DR EMBL; M37218; AAA98158.1; -;
DR PIR; S10921; S10921.
DR InterPro; IPR003059; Lysis_col.
DR Pfam; PF02402; Lysis_col; 1.
DR PRISM; PR01297; LYSISCOLICIN.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW PLASMID; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 45
FT LIPID 18 18
SQ SEQUENCE 45 AA; 4831 MW; A34D232FBC12B99D CRC64;

Query Match 87.5%; Score 21; DB 1; Length 45;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 29 GTVAPS 34

RESULT 31
LYS2_ECOLI STANDARD; PRT; 47 AA.
AC P06963;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicins E2 and E3 precursor.
GN HIC OR CELB.

OS Escherichia coli.
OG plasmid Cole2-P9, and plasmid Cole3-CA38.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.

OX NCBI_TaxID=562;
[1]

SEQUENCE FROM N.A.

RP PLASMID-Cole2-P9;
RC PLASMID-Cole2-P9;
RX MEDLINE=86195936; PubMed=3516985;

RA Toba M., Masaki H., Ohta T.;

RT "Primary structures of the Cole2-P9 and Cole3-CA38 lysis genes.";
RL J. Biochem. 99:591-596(1986).
[2]

SEQUENCE FROM N.A.

RP PLASMID-Cole2-P9;
RC PLASMID-Cole2-P9;
RX MEDLINE=85239907; PubMed=3892228;

RA Cole S.T., Saint-Joanis B., Pugsley A.P.;

RT "Molecular characterisation of the colicin E2 operon and
RT identification of its products.";
RL Mol. Gen. Genet. 198:465-472(1985).
[3]

SEQUENCE FROM N.A.

RP PLASMID-Cole3-CA38;
RC PLASMID-Cole3-CA38;
RX MEDLINE=85028427; PubMed=6092219;

RA Watson R.J., Lau P.C.K., Vernet T., Visentin L.P.;

RT "Characterization and nucleotide sequence of a colicin-release gene
RT in the hic region of plasmid Cole3-CA38.";
RL Gene 29:175-184(1984).
[4]

ERRATUM.

RP PLASMID-Cole3-CA38;

RA Watson R.J., Lau P.C.K., Vernet T., Visentin L.P.;

RL Gene 42:351-353(1986).
[5]

SEQUENCE OF 1-38 FROM N.A.

RP PLASMID-Cole3-CA38;

RC PLASMID-Cole3-CA38;

RX MEDLINE=85210906; PubMed=3889348;

RA Masaki H., Ohta T.;

RT "Colicin E3 and its immunity genes.";

RL J. Mol. Biol. 182:217-227(1985).

CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
AND PARTIAL CELL LYSIS.

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DR EMBL; X02397; CAA26243.1; -;
DR EMBL; D00020; BAA00014.1; -;

DR EMBL: D00021; BAA00015.1; -;
DR EMBL: J01574; AAA86419.1; -;
DR EMBL: X03631; CAA27281.1; -;
DR EMBL: X03632; CAA27282.1; -;
DR EMBL: M29885; AAA23070.1; -;
DR PIR: A22383; BVECH8.
DR PIR: JS0004; JS0004.
DR PIR: JS0529; JS0529.
DR InterPro: IPR003059; Lysis_col.
DR Pfam: PF02402; Lysis_col; 1.
DR PRINTS: PR01297; LYSISCOLICIN.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 47 LYSIS PROTEIN FOR COLICINS E2 AND E3.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 47 AA; 4860 MW; 691E149A8A164A0A CRC64;

Query Match 87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 31 GTVSPS 36

RESULT 32
LYS5_ECOLI
ID LYS5_ECOLI STANDARD; PRT; 47 AA.
AC PL3344;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E5 precursor.
GN Lys.
OS Escherichia coli.
OG Plasmid ColE5-099.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89364708; PubMed=2549375;
RA Lau P.C.K., Condie J.A.;
RT "Nucleotide sequences from the colicin E5, E6 and E9 operons:
RT presence of a degenerate transposon-like structure in the ColE9-J
RT plasmid.";
RL Mol. Gen. Genet. 217:269-277(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218006; PubMed=2561131;
RA Curtis M.D., James R., Coddington A.;
RT "An evolutionary relationship between the Cole5-099 and the Cole9-J
RT plasmids revealed by nucleotide sequencing.";
RL J. Gen. Microbiol. 135:2783-2788(1989).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
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DR EMBL: X15857; CAA33861.1; -;
DR EMBL: M30445; AAA98053.1; -;
DR PIR: JQ0330; JQ0330.
DR PIR: C45799; C45799.
DR InterPro: IPR003059; Lysis_col.

DR Pfam: PF02402; Lysis_col; 1.
DR PRINTS: PR01297; LYSISCOLICIN.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 47 LYSIS PROTEIN FOR COLICIN E5.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 47 AA; 4926 MW; 69133B25CA15A4B8 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 31 GTVSPS 36

RESULT 33
LYS6_ECOLI
ID LYS6_ECOLI STANDARD; PRT; 47 AA.
AC PL3345;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E6 precursor.
GN Lys.
OS Escherichia coli.
OG Plasmid ColE6-CT14.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89364708; PubMed=2549375;
RA Lau P.C.K., Condie J.A.;
RT "Nucleotide sequences from the colicin E5, E6 and E9 operons:
RT presence of a degenerate transposon-like structure in the ColE9-J
RT plasmid.";
RL Mol. Gen. Genet. 217:269-277(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90078082; PubMed=2687234;
RA Akutsu A., Masaki H., Ohta T.;
RT "Molecular structure and immunity specificity of colicin E6, an
RT evolutionary intermediate between E-group colicins and cloacin
RT DF13.";
RL J. Bacteriol. 171:6430-6436(1989).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
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DR EMBL: X15856; CAA33858.1; -;
DR EMBL: M31808; AAA23083.1; -;
DR PIR: JQ0328; JQ0328.
DR PIR: D43716; D43716.
DR InterPro: IPR003059; Lysis_col.
DR Pfam: PF02402; Lysis_col; 1.
DR PRINTS: PR01297; LYSISCOLICIN.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 47 LYSIS PROTEIN FOR COLICIN E6.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 47 AA; 4902 MW; 691E124F6A057ED8 CRC64;

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Query Match      87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 31 GTVSPS 36

RESULT 34
LVS9_ECOLI
ID LVS9_ECOLI STANDARD; PRT; 47 AA.
AC Q03709;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E7 precursor.
GN LYS OR CELE7.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91259043; PubMed=2045785;
RA Chak K.F., Kuo W.S., Lu F.M., James R.;
RT "Cloning and characterization of the Cole7 plasmid.";
RL J. Gen. Microbiol. 137:91-100(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-K317;
RA Lau P.C.K., Parsons M.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
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CC -----
DR EMBL; M57540; AAA23072.1; -.
DR InterPro; IPR003059; Lysis_col.
DR Pfam; PF02402; Lysis_col; 1.
DR PRINTS; PR01297; LYSISCOLICIN.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 47 LYSIS PROTEIN FOR COLICIN E7.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 47 AA; 4874 MW; 6900F2A17A057ED8 CRC64;

Query Match      87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 31 GTVSPS 36

RESULT 35
LVS8_ECOLI
ID LVS8_ECOLI STANDARD; PRT; 47 AA.
AC P10099;

Query Match      87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 31 GTVSPS 36

RESULT 36
LVS9_ECOLI
ID LVS9_ECOLI STANDARD; PRT; 47 AA.
AC P15176;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E9 precursor.
GN LYS.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;

Query Match      87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 31 GTVSPS 36

RESULT 37
LVS9_ECOLI
ID LVS9_ECOLI STANDARD; PRT; 47 AA.
AC P15176;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin E9 precursor.
GN LYS.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
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RN SEQUENCE FROM N.A.
RA Lau P.C.K.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88034907; PubMed=3312476;
RA James R., Jarvis M., Barker D.F.;
RT "Nucleotide sequence of the immunity and lysis region of the Cole9-J
RT plasmid.";
RL J. Gen. Microbiol. 133:1553-1562(1987).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
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CC -----
CC EMBL: X15858; CAA33866.1; -.
CC PIR: M16803; AAA23079.1; -.
CC InterPro: IPR003059; Lysis_col.
CC Pfam: PF02402; Lysis_col; 1.
CC PRINTS: PR01297; LYSISCOLICIN.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 47 LYSIS PROTEIN FOR COLICIN E9.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 47 AA; 4816 MW; 69062F749A057ED8 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 47;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 31 GTVSPS 36

RESULT 37
LYS0_ECOLI
ID LYS0_ECOLI STANDARD; PRT; 49 AA.
AC P02987;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein precursor (Protein H).
GN H OR CEX.
OS Escherichia coli.
OG Plasmid Clo DF13.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86314306; PubMed=3749334;
RA Nijkamp H.J., de Lang R., Stuitje A.R., van den Elsen P.J.M.,
RA Veltkamp E., van Putten A.J.;
RT "The complete nucleotide sequence of the bacteriocinogenic plasmid
RT CloDF13.";
RL Plasmid 16:135-160(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81148852; PubMed=6163089;
RA Stuitje A.R., Spelt C.E., Veltkamp E., Nijkamp H.J.J.;
RT "Identification of mutations affecting replication control of plasmid
RT Clo DF13.";
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```

RL Nature 290:264-267(1981).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
CC -!- MISCELLANEOUS: PLASMID CLO DF13 ORIGINATES FROM ENTEROBACTER
CC CLOACAE BUT IS STABLY MAINTAINED IN AND STUDIED MOSTLY FROM
CC E.COLI.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X04466; CAA28145.1; -.
CC PIR: A03515; ZHECP3.
CC InterPro: IPR003059; Lysis_col.
CC Pfam: PF02402; Lysis_col; 1.
CC PRINTS: PR01297; LYSISCOLICIN.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Plasmid; Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 49 LYSIS PROTEIN.
FT LIPID 22 22 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 49 AA; 5157 MW; 1A3DC979EBB0C5DC CRC64;

Query Match 87.5%; Score 21; DB 1; Length 49;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 33 GTVAPS 38

RESULT 38
LYS4_ECOLI
ID LYS4_ECOLI STANDARD; PRT; 52 AA.
AC P09181;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysis protein for colicin N precursor.
GN CNL.
OS Escherichia coli.
OG Plasmid ColN pCHAP4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12; PubMed=3280946;
RX MEDLINE=88174431; PubMed=3280946;
RA Pugsley A.P.;
RT "The immunity and lysis genes of ColN plasmid pCHAP4.";
RL Mol. Gen. Genet. 211:335-341(1988).
CC -!- FUNCTION: LYSIS PROTEINS ARE REQUIRED FOR BOTH COLICIN RELEASE
CC AND PARTIAL CELL LYSIS.
CC -----
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CC -----
CC EMBL: X06933; CAA30019.1; -.
CC PIR: S01760; ZHECNA.
CC InterPro: IPR003059; Lysis_col.
CC Pfam: PF02402; Lysis_col; 1.
```



```
QY 1 gtxxps 6
Db 12 GTETPS 17

RESULT 41
TRH4_ECOLI STANDARD; PRT; 118 AA.
AC Q00130;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRAH protein.
GN TRAH.
OS Escherichia coli.
OG Plasmid Inc-beta RP4.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RC STRAIN=HB101;
RX MEDLINE=92190548; PubMed=1665997;
RA Ziegler G., Pansegrau W., Strack B., Balzer D., Kroeger M.,
RA Kruff V., Lanka E.;
RT "Nucleotide sequence and organization of genes flanking the transfer
RT origin of promiscuous plasmid RP4.";
RL DNA Seq. 1:303-327(1991).
CC -!- FUNCTION: THE INITIATION PROCESS OF TRANSFER DNA SYNTHESIS
CC REQUIRES THE INTERACTION OF AT LEAST THREE PLASMID-SPECIFIC
CC COMPONENTS (TRAH, I, AND J) AT THE TRANSFER ORIGIN RESULTING
CC IN THE ASSEMBLY OF A SPECIALISED NUCLEOPROTEIN COMPLEX - THE
CC RELAXOSOME.
CC -----
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CC -----
CC EMBL; X54459; CAA38335.1; -.
DR PIR; S23000; S23000.
KW Plasmid; Conjugation.
FT INIT_MET 0
SQ SEQUENCE 118 AA; 12738 MW; 2FC1445479E6F4B6 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
Db 37 GTLAPS 42

RESULT 42
RK14_PORPU STANDARD; PRT; 122 AA.
AC P51304;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chloroplast 50S ribosomal protein L14.
GN RPL14.
OS Porphyra purpurea.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 87.5%; Score 21; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
Db 37 GTLAPS 42

RESULT 43
FMF7_ECOLI STANDARD; PRT; 170 AA.
AC P25394;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE F107 fimbrial protein precursor.
GN FEBA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=107/86;
RX MEDLINE=92225617; PubMed=1348723;
RA Imberechts H.A., de Greve H., Schlicker C., Bouchet H., Pohl P.,
RA Charlier G., Vandekerckhove J., van Damme J., van Montagu M.,
RA Lintermans P.;
RT "Characterization of F107 fimbriae of Escherichia coli 107/86, which
RT causes edema disease in pigs, and nucleotide sequence of the F107
RT major fimbrial subunit gene, fedA.";
RL Infect. Immun. 60:1963-1971(1992).
CC -!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -!- SUBCELLULAR LOCATION: Fimbria.
CC -----
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CC -----
CC EMBL; U38804; AAC08190.1; -.
DR HSSP; P04450; 1WHI.
DR Mendel; I0314; PORPU.rpl14; 1.
DR InterPro; IPR000218; Ribosomal_L14.
DR Pfam; PF00238; Ribosomal_L14; 1.
DR ProDom; PD001093; Ribosomal_L14; 1.
DR PROSITE; PS00049; RIBOSOMAL_L14; 1.
KW Ribosomal protein; Chloroplast.
SQ SEQUENCE 122 AA; 13411 MW; 49892C2AB0B6BEB2 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 122;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
Db 26 GTSNPS 31
```

DR EMBL; M61713; AAA23735.1; -.
DR EMBL; M61713; AAA23734.1; -.
DR PIR; A43841; A43841.
DR InterPro; IPR000259; Fimbrial.
DR Pfam; PF00419; Fimbrial; 1.
KW Fimbrial; Signal.
FT SIGNAL 1 21
FT CHAIN 22 170 F107 FIMBRIAL PROTEIN.
FT DISULFID 37 78 PROBABLE.
FT SEQUENCE 170 AA; 17329 MW; AF40947CE387692F CRC64;
SQ SEQUENCE 170 AA; 17329 MW; AF40947CE387692F CRC64;
Query Match 87.5%; Score 21; DB 1; Length 170;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 gtxxps 6
DB 54 GTVAPS 59
RESULT 44
OM24_ARATH
ID OM24_ARATH STANDARD; PRT; 187 AA.
AC P82805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitochondrial import receptor subunit TOM20-4 (Translocase of outer
DE membrane 20 kDa subunit 4).
OS Arabidopsis thaliana (Mouse-ear cress).
GN TOM20-4 OR AT5G40930 OR MMG1.2.
GC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016721; PubMed=11130714;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Kirchoff K., Toth K., King L., Bahret R., Wilson R.K., Bancroft I.,
RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Entian K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
RA Langham S.A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Ramsperger U., Wedler K., Balke K., Wedler E., Peters S.,
RA van Staveren M., Dirks W., Mooijman P., Klein Lankhorst R.,
RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
RA Feldpausch M., Lamberth S., Villarreal J., Gielen J., Ardiles W.,
RA Bents O., Lencke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
RA Schueller C., Zaccaria P., Meves H.-W., Bevan M., Fransch P.F.;
RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:823-826(2000).
[2]
RP SEQUENCE OF 102-117.
RC STRAIN=CV. COLUMBIA;
RX PubMed=11161051;
RA Werhahn W., Nlemeyer A., Jaensch L., Kruff V., Schmitz U.K.,
RA Braun H.-P.;

"Purification and characterization of the preprotein translocase of
the outer mitochondrial membrane from Arabidopsis thaliana.
Plant Physiol. 125:943-954(2001).
-!- FUNCTION: CENTRAL COMPONENT OF THE RECEPTOR COMPLEX RESPONSIBLE
FOR THE RECOGNITION AND TRANSLLOCATION OF CYTOSOLICALLY SYNTHESIZED
MITOCHONDRIAL PREPROTEINS. TOGETHER WITH TOM22 FUNCTIONS AS THE
TRANSIT PEPTIDE RECEPTOR AT THE SURFACE OF THE MITOCHONDRION
OUTER MEMBRANE AND FACILITATES THE MOVEMENT OF PREPROTEINS INTO
THE TRANSLLOCATION PORE.
-!- SUBUNIT: FORMS PART OF MITOCHONDRIAL RECEPTOR COMPLEX.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
outer membrane.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- MISCELLANEOUS: THERE ARE FOUR GENES (TOM20-1, TOM20-2, TOM20-3 AND
TOM20-4) WHICH ENCODE MITOCHONDRIAL IMPORT RECEPTOR SUBUNITS
TOM20.
-!- SIMILARITY: BELONGS TO THE TOM20 FAMILY.

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EMBL; AB023040; BAB10523.1; .
KW Transport; Protein transport; Outer membrane; Mitochondrion;
KW Transmembrane.
FT DOMAIN 1 160 INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 161 178 POTENTIAL.
FT DOMAIN 179 187 CYTOPLASMIC (POTENTIAL).
FT SEQUENCE 187 AA; 20973 MW; 156DF3D231EA286C CRC64;
SQ SEQUENCE 187 AA; 20973 MW; 156DF3D231EA286C CRC64;
Query Match 87.5%; Score 21; DB 1; Length 187;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 gtxxps 6
DB 137 GTAGPS 142
RESULT 45
Y319_MYCPN
ID Y319_MYCPN STANDARD; PRT; 193 AA.
AC P75329;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG319 homolog (H08_orf193).
GN MPN454 OR MP387.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OC NCBI_TaxID=2104;
[1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).

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CC -----

CC EMBL; AF000037; AAB96035.1; -

CC Hypothetical protein; Transmembrane; Complete proteome.

KW TRANSMEM 10 30 POTENTIAL.

FT TRANSMEM 136 156 POTENTIAL.

SQ SEQUENCE 193 AA; 21443 MW; BAE6806C6D80C1D CRC64;

Query Match 87.5%; Score 21; DB 1; Length 193;

Best Local Similarity 66.7%; Pred. No. 91;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

DB 31 GIVSPS 36

RESULT 46

COX3_MYCTU STANDARD; PRT; 203 AA.

AC Q10385;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable cytochrome c oxidase polypeptide III (EC 1.9.3.1) (Cytochrome

DE AA3 subunit 3).

GN CTA6 OR RV2193 OR MT2249 OR MTCY190.04.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,

RA Horsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skellton S., Squares R., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence.";

RL Nature 393:537-544 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.B.,

RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

RA Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and

RT laboratory strains.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SUBCELLULAR LOCATION: THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.

CC -----

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CC -----

CC EMBL; Z70283; CAA94262.1; -

DR EMBL; AE007071; AAK46535.1; -

DR HSP; P00415; LOCC.

DR TIGR; MT2249; -

DR Tuberculin; RV2193; -

DR InterPro; IPR000298; CytC_oxdse_III.

DR Pfam; PF00510; COX3; 1.

DR PROSITE; PS0253; COX3; 1.

KW Oxidoreductase; Transmembrane; Complete proteome.

FT TRANSMEM 30 50 POTENTIAL.

FT TRANSMEM 71 91 POTENTIAL.

FT TRANSMEM 96 116 POTENTIAL.

FT TRANSMEM 143 163 POTENTIAL.

FT TRANSMEM 179 199 POTENTIAL.

SQ SEQUENCE 203 AA; 22420 MW; 70145380A05BD0C2 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 203;

Best Local Similarity 66.7%; Pred. No. 95;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6

DB 128 GTSIPS 133

RESULT 47

NODB_RHISN STANDARD; PRT; 215 AA.

AC P50355;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Chitoooligosaccharide deacetylase (EC 3.5.1.-) (Modulation protein B).

GN NODB OR Y4HH.

OS Rhizobium sp. (strain NGR234).

OG Plasmid sym pNGR234a.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=394;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97305956; PubMed=9163424;

RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,

RA Perret X.;

RT "Molecular basis of symbiosis between Rhizobium and legumes.";

RL Nature 387:394-401 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95075295; PubMed=7984092;

RA Relic B., Perret X., Estrada-Garcia M.T., Kocinska J., Golinowski W.,

RA Krishnan H.B., Pueppke S.G., Broughton W.J.;

RT "Nod factors of Rhizobium are a key to the legume door.";

RL Mol. Microbiol. 13:171-178 (1994).

CC -!- FUNCTION: IS INVOLVED IN GENERATING A SMALL HEAT-STABLE COMPOUND

CC (NOD), AN ACETYL OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT

CC STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.

CC -----

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CC -----

CC EMBL; X73362; CAA51773.1; -

DR EMBL; AE000076; AAB91696.1; -

DR InterPro; IPR002509; Polysac_deacet.

DR Pfam; PF01522; Polysac_deacet; 1.

KW Hydrolase; Nodulation; Plasmid.

FT CONFLICT 148 149 RP -> S (IN REF. 2).

SO SEQUENCE 215 AA; 23625 MW; 8A91E2B4E9D6D57F CRC64;

Query Match 87.5%; Score 21; DB 1; Length 215;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 14 GTGAPS 19

RESULT 48

XYN2 ASPNG STANDARD; PRT; 225 AA.
AC P55330; 012557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.

OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IFO 4066;

RA Ito K.;

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
linkages in xylans.

CC -1- PATHWAY: XLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
HYDROLASES).

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CC EMBL; D38071; BAA07265.1; -

DR HSSP; P09850; 1XNB.

DR InterPro; IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Xylan degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 18 POTENTIAL.

FT PROPEP 19 37

FT CHAIN 38 225

FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).

SQ SEQUENCE 225 AA; 24057 MW; C4B8BB007AB2B8FD CRC64;

Query Match 87.5%; Score 21; DB 1; Length 225;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 99 GTFTPS 104

RESULT 49

PDXJ_NEIMA STANDARD; PRT; 242 AA.
ID PDXJ_NEIMA

AC Q9RQV9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyridoxal phosphate biosynthetic protein pdxJ.
GN PDXJ OR NMA2037.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RA Linz B., Schenker M., Achtman M.;

RT "Frequent horizontal genetic exchange between Neisseria meningitidis
and commensal neisseriae";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491";
RL Nature 404:502-506(2000).

CC -1- FUNCTION: CATALYZES THE CONDENSATION OF 1-DEOXY-D-XYLULOSE-5-
PHOSPHATE (DXP) AND 1-AMINO-3-OXO-4-(PHOSPHOHYDROXY)PROPAN-2-ONE
TO FORM PYRIDOXINE 5'-PHOSPHATE (PNP) (BY SIMILARITY).

CC -1- PATHWAY: DE NOVO SYNTHESIS OF PYRIDOXINE (VITAMIN B6) AND
PYRIDOXAL PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -1- SIMILARITY: BELONGS TO THE PDXJ FAMILY.

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or send an email to license@isb-sib.ch).

CC EMBL; AF058689; AAF06688.1; -

DR EMBL; AL162757; CAB85256.1; -

KW Pyridoxine biosynthesis; Complete proteome.

SQ SEQUENCE 242 AA; 26669 MW; 07AC9E95DDA8D090 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 242;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 18 GTTTPS 23

RESULT 50

PDXJ_NEIMB STANDARD; PRT; 242 AA.
ID PDXJ_NEIMB

AC Q9K0V9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Pyridoxal phosphate biosynthetic protein pdxJ.

GN PDXJ OR NMB0448.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=491;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=2017555; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: CATALYZES THE CONDENSATION OF 1-DEOXY-D-XYLULOSE-5-
CC PHOSPHATE (DXP) AND 1-AMINO-3-OXO-4-(PHOSPHOHYDROXY)PROPAN-2-ONE
CC TO FORM PYRIDOXINE 5'-PHOSPHATE (PNP) (BY SIMILARITY).
CC -!- PATHWAY: DE NOVO SYNTHESIS OF PYRIDOXINE (VITAMIN B6) AND
CC PYRIDOXAL PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE PDJX FAMILY.
CC -----
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CC -----
DR EMBL; AE002401; AAF40885.1; -.
DR TIGR; NMB0448; -.
KW Pyridoxine biosynthesis; Complete proteome.
SQ SEQUENCE 242 AA; 26565 MW; 5DA0476728AA1485 CRC64;

Query Match 87.5%; Score 21; DB 1; Length 242;
Best Local Similarity 66.7%; Pred. NO. 1.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 qtxxps 6
Db 18 GTTYPs 23

Search completed: September 3, 2002, 09:29:46
Job time: 228 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 3, 2002, 09:25:33 ; Search time 25.06 Seconds
(without alignments)
41.419 Million cell updates/sec

Title: BASK-853-CLAIM5

Perfect score: 24

Sequence: 1 gtxxps 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL_19.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	91.7	71	15	Q9IF05 human immun
2	22	91.7	75	10	Q41118 phaseolus v
3	22	91.7	80	15	Q90QH8 human immun
4	22	91.7	89	16	Q9HWZ4 pseudomonas
5	22	91.7	92	15	Q38158 human immun
6	22	91.7	93	15	Q38175 human immun
7	22	91.7	93	15	Q38177 human immun
8	22	91.7	96	15	Q38114 human immun
9	22	91.7	96	15	Q38161 human immun
10	22	91.7	96	15	Q38178 human immun
11	22	91.7	99	15	Q38030 human immun
12	22	91.7	99	15	Q38362 human immun
13	22	91.7	99	15	Q38371 human immun
14	22	91.7	99	15	Q38372 human immun
15	22	91.7	101	15	Q38113 human immun
16	22	91.7	101	15	Q38128 human immun

17	22	91.7	101	15	Q38130	Q38130 human immun
18	22	91.7	101	15	Q38133	Q38133 human immun
19	22	91.7	101	15	Q38138	Q38138 human immun
20	22	91.7	101	15	Q38141	Q38141 human immun
21	22	91.7	105	17	Q9YA39	Q9YA39 aeropyrum p
22	22	91.7	111	15	Q38165	Q38165 human immun
23	22	91.7	111	15	Q38166	Q38166 human immun
24	22	91.7	111	15	Q38169	Q38169 human immun
25	22	91.7	111	15	Q38171	Q38171 human immun
26	22	91.7	112	15	Q75698	Q75698 human immun
27	22	91.7	135	11	Q64053	Q64053 mus sp. orf
28	22	91.7	142	11	Q9D5C6	Q9D5C6 mus musculu
29	22	91.7	156	4	Q9HBN7	Q9HBN7 homo sapien
30	22	91.7	157	4	Q9NWG3	Q9NWG3 homo sapien
31	22	91.7	175	5	Q9VSO7	Q9VSO7 drosophila
32	22	91.7	177	12	Q41995	Q41995 maize rayad
33	22	91.7	178	2	Q9KY82	Q9KY82 streptomyce
34	22	91.7	182	5	Q9VSQ6	Q9VSQ6 drosophila
35	22	91.7	186	4	Q9BZ94	Q9BZ94 homo sapien
36	22	91.7	196	10	Q82664	Q82664 arabidopsis
37	22	91.7	200	2	Q9F5I3	Q9F5I3 agrobacteri
38	22	91.7	202	16	Q9KOL1	Q9KOL1 vibrio chol
39	22	91.7	218	11	Q9JLH5	Q9JLH5 rattus norv
40	22	91.7	228	2	Q9RDK2	Q9RDK2 streptomyce
41	22	91.7	233	2	Q9KXV0	Q9KXV0 streptomyce
42	22	91.7	237	6	P79289	P79289 sus scrofa
43	22	91.7	247	2	Q9L203	Q9L203 streptomyce
44	22	91.7	253	2	Q9L126	Q9L126 streptomyce
45	22	91.7	253	4	Q43563	Q43563 homo sapien
46	22	91.7	254	16	Q9I170	Q9I170 pseudomonas
47	22	91.7	275	13	Q98TY7	Q98TY7 brachydanio
48	22	91.7	285	10	Q9MOA9	Q9MOA9 arabidopsis
49	22	91.7	288	2	Q3RNC9	Q3RNC9 bartonella
50	22	91.7	288	12	Q9DWD6	Q9DWD6 rat cytomeg

ALIGNMENTS

RESULT 1
Q9IF05 PRELIMINARY; PRT; 71 AA.
ID Q9IF05;
AC Q9IF05;
DC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1079;
RX MEDLINE=21443958; PubMed=11559796;
RA Peters S., Munoz M., Verly S., Sanchez-Merino V., Lopez-Galindez C.,
Perin L., Larder B., Cmarko D., Fakan S., Meylan P., Teleni A.;
RT "Resistance to Nucleoside Analog Reverse Transcriptase Inhibitors
Mediated by Human Immunodeficiency Virus Type 1 p6 Protein.";
DL J. Virol. 75:9644-9653(2001).
RR EMBL; AF282969; AAF87830.1; -.
FT NON_TER 1
SQ SEQUENCE 71 AA; 7870 MW; 033C600C7F7FBCF3 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 71;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|||
Db 39 STATPS 44

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RESULT 2
Q41118 ID Q41118 PRELIMINARY; PRT; 75 AA.
AC Q41118
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CHALCONE SYNTHASE MRNA (FRAGMENT).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RA Ryder T.B., Cramer C.L., Bell J.N., Robbins M.P., Dixon R.A.,
RA Lamb C.J.;
RT "Elicitor rapidly induces chalcone synthase mRNA in Phaseolus vulgaris
RT cells at the onset of the phytoalexin defense response.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5724-5728(1984).
DR EMBL; K02953; AAA33758.1; -.
DR InterPro: IPR001099; Chal_stil_synth.
DR Pfam: PF00195; Chal_stil_synth; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8800 MW; 243CBED889A4F207 CRC64;

Query Match 91.7%; Score 22; DB 10; Length 75;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 18 GTATPS 23

RESULT 3
Q90QH8 ID Q90QH8 PRELIMINARY; PRT; 80 AA.
AC Q90QH8
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaufmann G.R., Suzuki K., Cunningham P., Mukaide M., Kondo M.,
RA Imai M., Zaunders J., Cooper D.A.;
RT "Impact of HIV Type 1 Protease, Reverse Transcriptase, Cleavage Site,
RT and p6 Mutations on the Virological Response to Quadruple Therapy with
RT Saquinavir, Ritonavir, and Two Nucleoside Analogs.";
RL AIDS Res. Hum. Retroviruses 17:487-497(2001).
DR EMBL; AF322313; AAK66674.1; -.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 8942 MW; 72C5C3148E51E65D CRC64;

Query Match 91.7%; Score 22; DB 15; Length 80;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 48 GTTTPS 53

RESULT 4
Q9HWZ4 ID Q9HWZ4 PRELIMINARY; PRT; 89 AA.
AC Q9HWZ4
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN PA4033.
GN PA4033.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004820; AAG07420.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 89 AA; 9452 MW; BFD4EBF98897E7E4 CRC64;

Query Match 91.7%; Score 22; DB 16; Length 89;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 48 GTASPS 53

RESULT 5
O38158 ID O38158 PRELIMINARY; PRT; 92 AA.
AC O38158
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its GAG substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024054; AAB83833.1; -.
DR HSSP; P05888; 1AAF.
DR InterPro: IPR001878; Znf.CCHC.
DR Pfam: PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 92
SQ SEQUENCE 92 AA; 10403 MW; 27E1160C29F611EA CRC64;

Query Match 91.7%; Score 22; DB 15; Length 92;
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Best Local Similarity 66.7%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Znf_C2HC; 2.

Oy 1 gtxxps 6
|| ||
Db 72 GTTPS 77

RESULT 6
O38175 O38175 PRELIMINARY; PRT; 93 AA.
AC O38175;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during Indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024071; AAB83850.1; -.
DR HSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1 1
NON_TER 93 93
SQ SEQUENCE 93 AA; 10402 MW; 0E9FF4DC4129C73 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 93;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
|| ||
Db 73 GTATPS 78

RESULT 7
O38177 O38177 PRELIMINARY; PRT; 93 AA.
AC O38177;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during Indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024074; AAB83852.1; -.
DR HSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1 1
NON_TER 93 93
SQ SEQUENCE 93 AA; 10502 MW; 5615F69550DDA09D CRC64;

Query Match 91.7%; Score 22; DB 15; Length 93;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
|| ||
Db 73 GTATPS 78

RESULT 8
O38114 O38114 PRELIMINARY; PRT; 96 AA.
AC O38114;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during Indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024010; AAB83789.1; -.
DR HSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1 1
NON_TER 96 96
SQ SEQUENCE 96 AA; 10766 MW; 74A041FFD4FE3935 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 96;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 gtxxps 6
|| ||
Db 76 GTATPS 81

RESULT 9
O38161 O38161 PRELIMINARY; PRT; 96 AA.
AC O38161;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;

```

RX MEDLINE-97404676; PubMed-9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024057; AAB83836.1; -.
DR HSSP; P05888; 1A4F.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10824 MW; 74B74DFE73E93935 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 96;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 76 GTTTPS 81

RESULT 10
O38178 O38178 PRELIMINARY; PRT; 96 AA.
AC O38178;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE-97404676; PubMed-9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024057; AAB83853.1; -.
DR HSSP; P05888; 1A4F.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10794 MW; 74B756FFC3E93935 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 96;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 76 GTTTPS 81

RESULT 11
O38030 O38030 PRELIMINARY; PRT; 99 AA.
AC O38030;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 3;
RX MEDLINE-97404676; PubMed-9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF023926; AAB83860.1; -.
DR HSSP; P05888; 1A4F.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 11140 MW; 92348443928FDCC0 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 99;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||
Db 79 GTTTPS 84

RESULT 12
O38362 O38362 PRELIMINARY; PRT; 99 AA.
AC O38362;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 7;
RX MEDLINE-97404676; PubMed-9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024261; AAB83135.1; -.
DR HSSP; P05888; 1A4F.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 11063 MW; 9818C494BED11470 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 99;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
   || ||

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Db 79 GTATPS 84

RESULT 13
O38371 PRELIMINARY; PRT; 99 AA.
AC O38371;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 7;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024270; AAB83144.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 11092 MW; 9818C494BD1E1470 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 99;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
| | |
Db 79 GTATPS 84

RESULT 14
O38372 PRELIMINARY; PRT; 99 AA.
AC O38372;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 7;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024271; AAB83145.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 11092 MW; 9818C494BD1E1470 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 99;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
| | |
Db 79 GTATPS 84

RESULT 15
O38113 PRELIMINARY; PRT; 101 AA.
AC O38113;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024009; AAB83788.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11408 MW; 2EF1A3E5CF282854 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
| | |
Db 81 GTTTPS 86

RESULT 16
O38128 PRELIMINARY; PRT; 101 AA.
AC O38128;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
SQ SEQUENCE 101 AA; 11408 MW; 2EF1A3E5CF282854 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
| | |
Db 81 GTTTPS 86

RESULT 16
O38128 PRELIMINARY; PRT; 101 AA.
AC O38128;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
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RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024024; AAB83803.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF000098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11295 MW; EBD5B3278BF1D5FA CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 81 GTTTPS 86

RESULT 17
O38130 PRELIMINARY; PRT; 101 AA.
AC O38130;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.

OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RC STRAIN=PATIENT 4;

RX MEDLINE=97404676; PubMed=9261388;

RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,

RA Vasudevachari M.B., Salzman N.P.;

RT "Drug resistance during indinavir therapy is caused by mutations in

the protease gene and in its Gag substrate cleavage sites.";

RL J. Virol. 71:6662-6670(1997).

DR EMBL; AF024026; AAB83805.1; -.

DR HSSP; P05888; IAAF.

DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF000098; zf-CCHC; 2.

DR SMART; SM00343; Znf_C2HC; 2.

KW Zinc-finger.

FT NON_TER 1

FT NON_TER 101

SQ SEQUENCE 101 AA; 11408 MW; F7B36D60472BDE0 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 81 GTTTPS 86

RESULT 18
O38133 PRELIMINARY; PRT; 101 AA.
AC O38133;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.

OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RC SEQUENCE FROM N.A.

RX STRAIN=PATIENT 4;

RX MEDLINE=97404676; PubMed=9261388;

RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,

RA Vasudevachari M.B., Salzman N.P.;

RT "Drug resistance during indinavir therapy is caused by mutations in

the protease gene and in its Gag substrate cleavage sites.";

RL J. Virol. 71:6662-6670(1997).

DR EMBL; AF024029; AAB83808.1; -.

DR HSSP; P05888; IAAF.

DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF000098; zf-CCHC; 2.

DR SMART; SM00343; Znf_C2HC; 2.

KW Zinc-finger.

FT NON_TER 1

FT NON_TER 101

SQ SEQUENCE 101 AA; 11364 MW; F7B9D83A5781D5FA CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 81 GTATPS 86

RESULT 19

O38138

ID O38138 PRELIMINARY; PRT; 101 AA.

AC O38138;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE GAG PROTEIN (FRAGMENT).

GN GAG.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RC SEQUENCE FROM N.A.

RX STRAIN=PATIENT 4;

RX MEDLINE=97404676; PubMed=9261388;

RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,

RA Vasudevachari M.B., Salzman N.P.;

RT "Drug resistance during indinavir therapy is caused by mutations in

the protease gene and in its Gag substrate cleavage sites.";

RL J. Virol. 71:6662-6670(1997).

DR EMBL; AF024034; AAB83813.1; -.

DR HSSP; P05888; IAAF.

DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF000098; zf-CCHC; 2.

DR SMART; SM00343; Znf_C2HC; 2.

KW Zinc-finger.

FT NON_TER 1

FT NON_TER 101

SQ SEQUENCE 101 AA; 11478 MW; 02BB523A5781CEFB CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 81 GTATPS 86

RESULT 20

O38141

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ID O38141 PRELIMINARY; PRT; 101 AA.
AC O38141;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024037; AAB83816.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1 101
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 11379 MW; F7BB523A5781D5FA CRC64;

Query Match 91.7%; Score 22; DB 15; Length 101;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 81 GTATPS 86

RESULT 21
Q9YA39 PRELIMINARY; PRT; 105 AA.
ID Q9YA39;
AC Q9YA39;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE HYPOTHETICAL 11.3 KDA PROTEIN APE2100.
GN APE2100.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kavarabaysi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000063; BAAB111.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 105 AA; 11262 MW; B25D94F6CED05D87 CRC64;

Query Match 91.7%; Score 22; DB 17; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 gtxxps 6
DB 15 GTSSPS 20

RESULT 22
O38165 PRELIMINARY; PRT; 111 AA.
ID O38165;
AC O38165;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024061; AAB83840.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger.
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12601 MW; A3611A55B709F506 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
DB 91 GTTTS 96

RESULT 23
O38166 PRELIMINARY; PRT; 111 AA.
ID O38166;
AC O38166;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024062; AAB83841.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.

```

KW Zinc-finger. 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12684 MW; FC3BEFE25A1B7EDB CRC64;

Query Match 91.7%; Score 22; DB 15; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 91 GTTTPS 96

RESULT 24
O38169 PRELIMINARY; PRT; 111 AA.
AC O38169;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024065; AAB83844.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger. 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12684 MW; 39C82CAA0BADFDDE CRC64;

Query Match 91.7%; Score 22; DB 15; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 91 GTTTPS 96

RESULT 25
O38171 PRELIMINARY; PRT; 111 AA.
AC O38171;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG PROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 4;
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,

RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024067; AAB83846.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Zinc-finger. 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12482 MW; 653BE64427F9D8FC CRC64;

Query Match 91.7%; Score 22; DB 15; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 91 GTATPS 96

RESULT 26
Q75698 PRELIMINARY; PRT; 112 AA.
AC Q75698;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAG POLYPROTEIN (FRAGMENT).
GN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96213510; PubMed=8638406;
RA Barrie K.A., Perez E.E., Lamers S.L., Farmerie W.G., Dunn B.M.,
RA Sleasman J.W., Goodenow M.M.;
RT "Natural variation in HIV-1 protease, Gag p7 and p6, and protease
cleavage sites within gag/pol polyproteins: amino acid substitutions
in the absence of protease inhibitors in mothers and children infected
by human immunodeficiency virus type 1.";
RL Virology 219:407-416(1996).
DR EMBL; U53663; AAB05739.1; -.
DR HSSP; P05888; IAAF.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf-CCHC; 2.
DR SMART; SM00343; Znf_C2HC; 2.
KW Polyprotein; Zinc-finger.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12895 MW; C97021F2A4407CA7 CRC64;

Query Match 91.7%; Score 22; DB 15; Length 112;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
|| ||
Db 94 GTTTPS 99

RESULT 27
Q64053 PRELIMINARY; PRT; 135 AA.
AC Q64053;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ORF 5' OF FIBROBLAST GROWTH FACTOR RECEPTOR 1 FGFR-1.
GN Mus sp.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95100926; PubMed=7802632;
RA Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama S.,
RA Terakawa N., Kishimoto T., Sato B.;
RT "Murine fibroblast growth factor receptor 1 gene generates multiple
RT messenger RNAs containing two open reading frames via alternative
RT splicing.";
RL Biochem. Biophys. Res. Commun. 205:1057-1063(1994).
DR EMBL: S74765; AAB32844.2; -
DR MGD; MGI:95522; Fgfr1.
KW Receptor.
SQ SEQUENCE 135 AA; 14280 MW; 03906AD6DC40880F CRC64;

Query Match 91.7%; Score 22; DB 11; Length 135;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 105 GTAAPS 110

RESULT 28
Q9D5C6 PRELIMINARY; PRT; 142 AA.
AC Q9D5C6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 4930465A12RIK PROTEIN.
GN 4930465A12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK015502; BAB29872.1; -
DR MGD; MGI:1922239; 4930465A12RIK.
SQ SEQUENCE 142 AA; 15397 MW; AF4B8868A17B745E CRC64;

Query Match 91.7%; Score 22; DB 11; Length 142;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 74 GTATPS 79

RESULT 29
Q9HBN7 PRELIMINARY; PRT; 156 AA.
AC Q9HBN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 16.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.O., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel Human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218021; AAG17263.1; -
KW Hypothetical protein.
SQ SEQUENCE 156 AA; 16178 MW; 183180BEC8F93E63 CRC64;

Query Match 91.7%; Score 22; DB 4; Length 156;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
Db 10 GTAAPS 15

RESULT 30
Q9NWX3 PRELIMINARY; PRT; 157 AA.
AC Q9NWX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 17.4 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=EMBRIO;
RA Isoqai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Konai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000905; BAA91418.1; -
SQ SEQUENCE 157 AA; 17352 MW; 2B1C874775BC2D23 CRC64;

Query Match 91.7%; Score 22; DB 4; Length 157;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

Db 76 GTAAPS 81

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RESULT 31
Q9VSO7 PRELIMINARY; PRT; 175 AA.
AC Q9VSO7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG13309 PROTEIN.
GN CG13309.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003554; AAF50359.1; -.
DR FlyBase; FBgn0035933; CG13309.
SQ SEQUENCE 175 AA; 18038 MW; A094BA899ADFA1C7 CRC64;
```

Query Match 91.7%; Score 22; DB 5; Length 175;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 98 GTSTPS 103

RESULT 32

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O41995 PRELIMINARY; PRT; 177 AA.
AC O41995;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE COAT PROTEIN (FRAGMENT).
OS maize rayado fino virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Marafivirus.
OX NCBI_TaxID=59749;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UNITED STATES;
RX MEDLINE=98062136; PubMed=9400964;
RA Hammond R.W., Kogel R., Ramirez P.;
RT "Variability of geographically distinct isolates of maize rayado fino virus in Latin America.";
RL J. Gen. Virol. 78:0-0(0).
DR EMBL; U97729; AAB96574.1; -.
DR InterPro; IPR000574; Tymo_coat.
DR Pfam; PF00983; Tymo_coat; 1.
FT NON_TER 1
SQ SEQUENCE 177 AA; 18918 MW; F1A95271D011795E CRC64;
```

Query Match 91.7%; Score 22; DB 12; Length 177;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 171 GTATPS 176

RESULT 33

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Q9KY82 PRELIMINARY; PRT; 178 AA.
AC Q9KY82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HYPOTHETICAL 19.7 KDA PROTEIN.
GN SKJ15.22.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=97000351; PubMed=8843436;
RX Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL356813; CAB92613.1; -.
KW Hypothetical protein.
SQ SEQUENCE 178 AA; 19681 MW; 155BA91389A2DDE6 CRC64;
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Query Match 91.7%; Score 22; DB 2; Length 178;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 2 GTTSPS 7

RESULT 34
 Q9VSO6 PRELIMINARY; PRT; 182 AA.
 ID Q9VSO6
 AC Q9VSO6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CGI3308 PROTEIN.
 GN CGI3308.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bock J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003554; AAF50360.1; -;
 DR FlyBase; FBgn0035932; CGI3308.
 SQ SEQUENCE 182 AA; 18808 MW; 64B9775C44A3AEE2 CRC64;

Query Match 91.7%; Score 22; DB 5; Length 182;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 105 GTSPS 110

RESULT 35
 Q9BZ94 PRELIMINARY; PRT; 186 AA.
 ID Q9BZ94
 AC Q9BZ94
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ZINC FAMILY MEMBER 4 PROTEIN HZIC4.
 GN ZIC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MEDULLOBLASTOMA;
 RA Warder D.E.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF332509; AAK06845.1; -;
 DR HSSP; P08047; 1SP2.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; Znf-C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 186 AA; 20189 MW; BF4C37753D290527 CRC64;

Query Match 91.7%; Score 22; DB 4; Length 186;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
 || ||
 Db 67 GTATPS 72

RESULT 36
 O82664 PRELIMINARY; PRT; 196 AA.
 ID O82664
 AC O82664
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BLUE COPPER BINDING-LIKE PROTEIN (AT5G20230/F5024_120) (PUTATIVE BLUE
 DE COPPER BINDING PROTEIN).
 GN AWI 32 OR ATBCD.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANSBERG ERECTA;
 RA Honma T., Goto K.;
 RT "Characterization of a wound-inducible Arabidopsis gene encoding a
 RT protein homologous to blue copper binding proteins.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. LANSBERG ERECTA;
 RA Honma T., Goto K.;
 RT "The Arabidopsis floral homeotic gene PISTILLATA is regulated by
 RT discrete cis-elements responsive to induction and maintenance
 RT signals.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene P5024.120/AT5g20230";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18227; CAA77089.1; -;
 DR EMBL; AB035137; BAA86999.1; -;
 DR EMBL; AY052681; AAK96585.1; -;
 DR EMBL; AY034986; AAK59491.1; -;
 DR HSSP; P29602; 1JER.
 DR InterPro; IPR000923; Copper_blue1.
 DR InterPro; IPR003245; Cu_bind_like.
 DR Pfam; PF02298; Cu_bind_like; 1.
 DR ProDom; PD003122; Cu_bind_like; 1.
 DR ProSITE; PS00196; COPPER_BLUE; 1.
 SQ SEQUENCE 196 AA; 20053 MW; 05100B50518F0A56 CRC64;

Query Match 91.7%; Score 22; DB 10; Length 196;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || || ||

Db 158 GTTTPS 163

RESULT 37
 Q9F5I3 PRELIMINARY; PRT; 200 AA.
 AC Q9F5I3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE R1ORF4 PROTEIN.
 GN R1ORF4.
 OS Agrobacterium rhizogenes.
 OG Plasmid pRI1724.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=359;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01724;
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N.,
 RA Yoshida K.;
 RT "The complete nucleotide sequence of a Ri (root inducing) plasmid
 RT indicates its chimerical structure between ri and Sym plasmids.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01724;
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
 RT "Analysis of unique variable region of a plant root inducing plasmid,
 RT pRI1724, by the construction of its physical map and library.";
 [2]

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01724;
 RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
 RT "Genome structure of Ri plasmid (1): Construction of linking library
 RT and physical map of pRI1724 in Japanese Agrobacterium.";
 RL Nucleic Acids Symp. Ser. 39:189-190(1998).
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01724;
 RX MEDLINE=20241294; PubMed=10780382;
 RA Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
 RA Yoshida K.;
 RT "Genome structure of Ri plasmid (1): Sequencing analysis of T-DNA and
 RT its flanking regions of pRI1724 in Japanese Agrobacterium
 RT rhizogenes.";
 RL Nucleic Acids Symp. Ser. 42:67-68(1999).
 CC -!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL; AF002086; BAB16123.1; -;
 DR InterPro; IPR000847; HTH_LysR.
 DR Pfam; PF00126; HTH_1; 1.
 KW DNA-binding; Plasmid; Transcription regulation.
 SQ SEQUENCE 200 AA; 21360 MW; 6888FA7699BFCEAF CRC64;

Query Match 91.7%; Score 22; DB 2; Length 200;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || || ||

Db 177 GTAAPS 182

RESULT 38
 Q9KQL1 PRELIMINARY; PRT; 202 AA.
 AC Q9KQL1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OUTER MEMBRANE LIPOPROTEIN SLP, PUTATIVE.
 GN VC1987.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004273; AAF95135.1; -;
 DR TIGR; VC1987; -;
 KW Lipoprotein; Complete proteome.
 SQ SEQUENCE 202 AA; 22661 MW; DA43B8A8D40DB691 CRC64;

Query Match 91.7%; Score 22; DB 16; Length 202;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || || ||

Db 134 GTTAPS 139

RESULT 39

Q9JLH5 ID Q9JLH5 PRELIMINARY; PRT; 218 AA.

AC Q9JLH5;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE CDK5 ACTIVATOR-BINDING PROTEIN.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2018474; PubMed=10721722;

RA Ching Y.P., Qi Z., Wang J.H.;

RT "Cloning of three novel neuronal Cdk5 activator binding proteins.";

RL Gene 242:285-294(2000).

DR EMBL; AF17478; AAF60224.1; -

SQ SEQUENCE 218 AA; 24023 MW; 2C6750AABA0D0EDA CRC64;

Query Match 91.7%; Score 22; DB 11; Length 218;

Best Local Similarity 66.7%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 209 GTSSPS 214

RESULT 40

Q9RDK2 ID Q9RDK2 PRELIMINARY; PRT; 228 AA.

AC Q9RDK2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE PUTATIVE MEMBRANE PROTEIN.

GN SCC123.22C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Brown S.P., Harris D.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RX MEDLINE=97000351; PubMed=8843436;

RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmid and a detailed genetic and physical map for

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).

DR EMBL; AL136518; CAB66262.1; -

SQ SEQUENCE 228 AA; 24246 MW; 6217C85671050B30 CRC64;

Query Match 91.7%; Score 22; DB 2; Length 228;

Best Local Similarity 66.7%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 206 GTATPS 211

RESULT 41

Q9KXV0

ID Q9KXV0 PRELIMINARY; PRT; 233 AA.

AC Q9KXV0;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE PUTATIVE SECRETED PROTEIN.

GN SCD95A.24.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Seeger K.J., Harris D.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RX MEDLINE=97000351; PubMed=8843436;

RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmid and a detailed genetic and physical map for

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).

DR EMBL; AL357432; CAB93051.1; -

SQ SEQUENCE 233 AA; 23071 MW; D3E0BEE9A356083D CRC64;

Query Match 91.7%; Score 22; DB 2; Length 233;

Best Local Similarity 66.7%; Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6

|| ||

Db 52 GTATPS 57

RESULT 42

P79289

ID P79289 PRELIMINARY; PRT; 237 AA.

AC P79289;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE SPL TRANSCRIPTION FACTOR (FRAGMENT).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=ENDOMETRIUM;

RX MEDLINE=20150569; PubMed=10687861;

RA Simmen R.C.M., Zhang X.L., Zhang D., Wang Y., Michel F.J.,

RA Simmen F.A.;

RT "Expression and regulatory function of the transcription factor Spl in
the uterine endometrium at early pregnancy: implications for
epithelial phenotype.";

RT Mol. Cell. Endocrinol. 159:159-170(2000).

DR EMBL: U57347; AAB39513.3; -.
 DR HSP: P08047; ISP2.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; zf-C2H2; 3.
 DR SMART: SM00355; Znf-C2H2; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 4.
 KW DNA-binding; Metal-binding; Zinc-finger.
 FT NON_TER 1
 FT NON_TER 237
 FT NON_TER 237
 SQ SEQUENCE 237 AA; 25421 MW; C6950DB42912DAB6 CRC64;

Query Match 91.7%; Score 22; DB 6; Length 237;
 Best Local Similarity 66.7%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 DB 204 GTATPS 209

RESULT 43
 Q9L203 PRELIMINARY; PRT; 247 AA.
 AC Q9L203;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE BIOTIN SYNTHASE.
 SC8E4.05C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; ALI38661; CAB71805.1; -.
 DR InterPro: IPR003784; BioY.
 DR Pfam: PF02632; BioY; 1.
 SQ SEQUENCE 247 AA; 24640 MW; 3A5EF99FDD7CF0CE CRC64;

Query Match 91.7%; Score 22; DB 2; Length 247;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 DB 150 GTAAPS 155

RESULT 44
 Q9L126 PRELIMINARY; PRT; 253 AA.
 ID Q9L126
 AC Q9L126;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PUTATIVE LIPOPROTEIN.
 GN SC6D11.30.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; ALI58061; CAB76353.1; -.
 KW Lipoprotein.
 SQ SEQUENCE 253 AA; 26600 MW; FECC3325A465D891 CRC64;

Query Match 91.7%; Score 22; DB 2; Length 253;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
 || ||
 DB 122 GTASPS 127

RESULT 45
 O43563 PRELIMINARY; PRT; 253 AA.
 ID O43563;
 AC O43563;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ORCTL25 HYPOTHETICAL PROTEIN.
 GN ORCTL25 OR BWR1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Cooper P.R., Smilnich N.J., Day C.D., Nowak N.J., Reid L.H.,
 RA Pearsall R.S., Reece M., Prawitt D., Landers J., Housman D.E.,
 RA Winterpacht A., Zabel B.O., Pelletier J., Weissman B.E., Shows T.B.,
 RA Higgins M.J.;
 RA Genomics 0:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98188297; PubMed=9520460;
 RA Schwenbacher C., Sabbioni S., Campi M., Veronese A., Bernardi G.,
 RA Menegatti A., Hataida I., Mukai T., Ohashi H., Barbanti-Brodano G.,
 RA Croce C.M., Negrini M.;
 RA "Transcriptional map of 170-kb region at chromosome 11p15.5:
 RT identification and mutational analysis of the BWR1A gene reveals the
 presence of mutations in tumor samples.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3873-3878(1998).
 DR EMBL; AF037066; AAC04789.1; -.

DR EMBL; AF035407; AAC17497.1; -;
SQ SEQUENCE 253 AA; 27218 MW; 183DE7B5C8A2255B CRC64;

Query Match 91.7%; Score 22; DB 4; Length 253;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 240 GTSTPS 245

RESULT 46

Q91170 ID Q91170 PRELIMINARY; PRT; 254 AA.
AC Q91170
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PROBABLE THIOESTERASE.
GN PA2411.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004668; AAG05799.1; -;
DR InterPro; IPR001031; thioesterase.
DR Pfam; PF00975; Thioesterase; 1.
KW Complete proteome.
SQ SEQUENCE 254 AA; 27878 MW; 460C521723BD7403 CRC64;

Query Match 91.7%; Score 22; DB 16; Length 254;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 108 GTAAPS 113

RESULT 47

Q98TY7 ID Q98TY7 PRELIMINARY; PRT; 275 AA.
AC Q98TY7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOD.
GN MYOD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao J., Du S.;
RT "Isolation and Characterization of Muscle-Specific Expression of

RT Zebrafish Myod Gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH AN OTHER
CC BHLH PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL; AF318503; AAK06755.1; -;
DR HSP; P10085; IMDY.
DR InterPro; IPR002546; Basic.
DR InterPro; IPR001092; HLH_dim.
DR InterPro; IPR003015; HLH_Myc.
DR Pfam; PF01586; Basic; 1.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00520; BASIC; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW DNA-binding
SQ SEQUENCE 275 AA; 30918 MW; 0A395542F95B37D8 CRC64;

Query Match 91.7%; Score 22; DB 13; Length 275;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 253 GTTAPS 258

RESULT 48

Q9M0A9 ID Q9M0A9 PRELIMINARY; PRT; 285 AA.
AC Q9M0A9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 30.9 KDA PROTEIN.
GN AT4G30510.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lanar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL161577; CAB79789.1; -;
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 285 AA; 30935 MW; E8E7017F494969E1 CRC64;

Query Match 91.7%; Score 22; DB 10; Length 285;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtxxps 6
|| ||
Db 233 GTSSPS 238

RESULT 49

Q9RNC9 ID Q9RNC9 PRELIMINARY; PRT; 288 AA.
AC Q9RNC9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VIRB9 HOMOLOG.
GN Bartonella
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOUSTON-1;
RX MEDLINE=20338084; PubMed=10882236;
RA Padmalayam I., Karem K., Baumstark B., Massung R.;
RT "The gene encoding the 17-kDa antigen of Bartonella henselae is
RT located within a cluster of genes homologous to the virB virulence
RT operon.";
RL DNA Cell Biol. 19:377-382(2000).
DR EMBL; AF182718; AAF0947.1; -. B94F15C58F38D489 CRC64;
SQ SEQUENCE 288 AA; 32120 MW; B94F15C58F38D489 CRC64;

Query Match 91.7%; Score 22; DB 2; Length 288;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
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Db 271 GTTSPS 276

RESULT 50
Q9DWD6
ID Q9DWD6 PRELIMINARY; PRT; 288 AA.
AC Q9DWD6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PR58.
GN R58.
OS Rat cytomegalovirus (strain Maastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE OF 1-168 FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=96335691; PubMed=8757999;
RA Beuken E., Slobbe R., Bruggeman C.A., Vink C.;
RT "Cloning and sequence analysis of the genes encoding DNA polymerase,
RT glycoprotein B, gp18.5 and major DNA-binding protein of rat
RT cytomegalovirus.";
RL J. Gen. Virol. 77:1559-1562(1996).
RN [2]
RP SEQUENCE OF 167-288 FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=98033207; PubMed=9367384;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Cloning and functional characterization of the origin of lytic-phase
RT DNA replication of rat cytomegalovirus.";
RL J. Gen. Virol. 78:2963-2973(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20473137; PubMed=11018281;
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a

RT spliced transcript.";
RL Virus Res. 69:119-130(2000).
DR EMBL; AF232689; AAF99154.1; -.
SQ SEQUENCE 288 AA; 30131 MW; C8F592D7837C9A34 CRC64;

Query Match 91.7%; Score 22; DB 12; Length 288;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtxxps 6
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Db 247 GTATPS 252

Search completed: September 3, 2002, 09:29:29
Job time: 236 sec

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